

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:41:09 ; Search time 38 Seconds
(without alignments)
2262.514 Million cell updates/sec

Title: US-10-043-787-1

Perfect score: 2271

Sequence: 1 MSDKLPYKVDIGLAAGRK.....QAQYLGMSCDGPFKPDHYRY 432

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2266	99.8	457	9	US-09-925-301-1059
2	1748	77.0	437	12	Sequence 5097, Ap
3	1733	76.3	433	12	Sequence 5097, Ap
4	1733	76.3	433	12	Sequence 2435, Ap
5	1633	71.9	449	12	Sequence 2430, Ap
6	1594	70.2	447	12	Sequence 1740, Ap
7	1546	68.1	426	12	Sequence 3683, Ap
8	1514.5	66.7	516	12	Sequence 10135, A
9	1465	64.5	468	12	Sequence 13111, A
10	1428	62.9	468	12	Sequence 10445, A
11	1422	62.6	468	12	Sequence 9241, Ap
12	1406	61.9	476	12	Sequence 9386, Ap
13	1405	61.9	466	12	Sequence 8266, Ap
14	1401	61.7	469	12	Sequence 8750, Ap
15	1401	61.7	469	12	Sequence 15745, A
					Sequence 16129, A

16	1399	61.6	463	12	US-10-369-493-19704	Sequence 19704, A
17	1393	61.3	469	12	US-10-314-657-71	Sequence 71, Appl
18	1372	60.4	485	15	US-10-156-761-12587	Sequence 12587, A
19	1357	59.8	461	12	US-10-369-493-21032	Sequence 21032, A
20	1355	59.7	461	12	US-10-369-493-4783	Sequence 4783, Ap
21	1355	59.7	461	12	US-10-369-493-7543	Sequence 7543, Ap
22	1342	59.1	446	12	US-10-369-493-17552	Sequence 17552, A
23	1340.5	59.0	463	12	US-10-369-493-7922	Sequence 7922, Ap
24	1336	58.8	459	12	US-10-369-493-10671	Sequence 10671, A
25	1311	57.7	446	12	US-10-369-493-15377	Sequence 15377, A
26	1310	57.7	463	12	US-10-369-493-20829	Sequence 20829, A
27	1302.5	57.4	466	12	US-10-369-493-19331	Sequence 19331, A
28	1300	57.2	465	12	US-10-369-493-17934	Sequence 17934, A
29	1296	57.1	461	12	US-10-369-493-11466	Sequence 11466, A
30	1296	57.1	461	12	US-10-369-493-14652	Sequence 14652, A
31	1296	57.1	464	12	US-10-369-493-15125	Sequence 15125, A
32	1296	57.1	466	12	US-10-369-493-12110	Sequence 12110, A
33	1256.5	55.3	463	12	US-10-369-493-16776	Sequence 16776, A
34	1242	54.7	478	11	US-09-746-660A-98	Sequence 98, Appl
35	1242	54.7	498	11	US-09-919-854-2	Sequence 2, Appl
36	1238	54.5	474	10	US-09-738-626-4336	Sequence 13881, A
37	1225.5	54.0	469	12	US-10-369-493-13881	Sequence 14175, A
38	1160	51.1	416	12	US-10-369-493-14175	Sequence 2, Appl
39	1151	50.7	614	9	US-09-782-051-2	Sequence 102, App
40	1098	48.3	432	11	US-09-746-660A-102	Sequence 90, Appl
41	943	41.5	418	12	US-10-369-493-30	Sequence 22854, A
42	927.5	40.8	399	12	US-10-369-493-22854	Sequence 9005, Ap
43	885	39.0	416	12	US-10-369-493-9005	Sequence 21670, A
44	878.5	38.7	422	12	US-10-369-493-21670	Sequence 1245, Ap
45	871.5	38.4	425	12	US-10-369-493-1245	

ALIGNMENTS

RESULT 1

US-09-925-301-1059
; Sequence 1059, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1059
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1059

Query Match 99.8%; Score 2266; DB 9; Length 457;
Best Local Similarity 99.8%; Pred. No. 3.6e-220;
Matches 431; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSDKLPYKVDIGLAAGRKALDIAENEMPGLMRRERYASAKPLKGARIAGCLHMTVET	60
Db	26	MSDKLPYKVDIGLAAGRKALDIAENEMPGLMRRERYASAKPLKGARIAGCLHMTVET	85
QY	61	AVLIETVLTGAEVQWSSCNIFSTQDHAAATAKAGIPYAWKGETDESYLWCIEQTLVF	120
Db	86	AVLIETVLTGAEVQWSSCNIFSTQDHAAATAKAGIPYAWKGETDESYLWCIEQTLVF	145
QY	121	KDGPLNMLDDGGDLTLNHTKYPQLLPGIRISSETTTGVNLYKMANGILKVPAINV	180
Db	146	KDGPLNMLDDGGDLTLNHTKYPQLLPGIRISSETTTGVNLYKMANGILKVPAINV	205

QY 181 NDSVTSKFDNLYGCRSLIDGIKRATDVMIAGKAVVAGYGVGKCAQALRGFGARVI 240
Db 206 NDSVTSKFDNLYGCRSLIDGIKRATDVMIAGKAVVAGYGVGKCAQALRGFGARVI 265
QY 241 ITEIDPINALQAAMEGYEVTMTDEACQEGNIFVTTTGCIDIIILGRHFEQMKDDAIVCNIG 300
Db 266 ITEIDPINALQAAMEGYEVTMTDEACQEGNIFVTTTGCIDIIILGRHFEQMKDDAIVCNIG 325
QY 301 HFDEIDVKWLNENAVEKNIKQVDYRLKNGRRILLAEGRVLNLCAMGHPSPFVMSN 360
Db 326 HFDEIDVKWLNENAVEKNIKQVDYRLKNGRRILLAEGRVLNLCAMGHPSPFVMSN 385
QY 361 SFTNQVMAQIELWTHDPKYPVGVHFLPKKLDEAVAHAHLGKLNVLTKLTEKQAQYLGMS 420
Db 386 SFTNQVMAQIELWTHDPKYPVGVHFLPKKLDEAVAHAHLGKLNVLTKLTEKQAQYLGMS 445
QY 421 CDGPFKPDHRY 432
Db 446 CDGPFKPDHRY 457

RESULT 2
US-10-369-493-5097
; Sequence 5097, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5097
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5097

Query Match 77.0%; Score 1748; DB 12; Length 437;
Best Local Similarity 76.7%; Pred. No. 8.2e-168;
Matches 332; Conservative 41; Mismatches 56; Indels 4; Gaps 2;

QY 4 KLPYKVDIGLAAGWKALDIAENEMPGMLMRERYASAKPLKGARIAGCLHMTVETAVL 63
Db 5 KPAYKVDIKLADFGKKEIILAENEMPGMLMAMRSKYGPQPLKGARIAGCLHMTIQTAVL 64
QY 64 IETLVLTGAEVQWSSCNIFSTQNHAAAAIAKAGIPVYAWKGETDEEYLWCIEQTLVFKDG 123
Db 65 IETLVLTGAEVQWSSCNIFSTQDHAAAAIAQTGPVYAWKGETDEEYLWCIEQTLVFKDG 124
QY 124 -PLANMILDDGGDLTNLIHTKYPOLLPGIRGISETTTGVHNLKYMANGILKVPAINVND 182
Db 125 QPLNMILDDGGDLTNLIHTKYPOLLPGIRGISETTTGVHNLAKMLAKGDLKVPAINVND 184
QY 183 SVTKSFDNLYGCRSLIDGIKRATDVMIAGKAVVAGYGVGKCAQALRGFGARVIIT 242
Db 185 SVTKSFDNLYGCRSLIDGIRKATDVMIAGKAVVAGYGVGKCAQALRGFGARVIIT 244
QY 243 EIDPINALQAAMEGYEVTMTDEACQEGNIFVTTTGCIDIIILGRHFEQMKDDAIVCNIGHF 302
Db 245 EIDPINALQAAMEGYEVTMTDEAAAPKANIIVTTTGCIDIVTGKFDIVTGKFDIVTGKFDIV 304
QY 303 DVEIDVKWLNENAVEKNIKQVDYRLKNGRRILLAEGRVLNLCAMGHPSPFVMSNSF 362
Db 305 DCEIDVKWLNENAVEKNIKQVDYRLKNGRRILLAEGRVLNLCAMGHPSPFVMSNSF 364

QY 363 TNQVMAQIELWTH---PKYVPVGVHFLPKKLDEAVAHAHLGKLNVLTKLTEKQAQYLG 419
Db 365 TNQVLAQVELWTKFGTPQBYKGLVYVLPKTLDEEVAYLHLAGVKLTKLSDEQASYLG 424
QY 420 SCDGPFKPDHRY 432
Db 425 PVAGPYKPDHRY 437

RESULT 3
US-10-369-493-2425
; Sequence 2425, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2425
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-2425

Query Match 76.3%; Score 1733; DB 12; Length 433;
Best Local Similarity 77.1%; Pred. No. 2.7e-166;
Matches 330; Conservative 40; Mismatches 56; Indels 2; Gaps 2;

QY 7 YKVADIGLAAGWKALDIAENEMPGMLMRERYASAKPLKGARIAGCLHMTVETAVLIET 66
Db 6 YKVADISLAAGWKALDIAENEMPGMLMRERYASAKPLKGARIAGCLHMTIQTAVLIET 65
QY 67 LVTGAEVQWSSCNIFSTQNHAAAAIAKAGIPVYAWKGETDEEYLWCIEQTLVFKDG-P 124
Db 66 LVALGAEVQWSSCNIFSTQDHAAAAIAATGVVPAWKGETDEEYLWCIEQTLVFKDG-P 125
QY 125 LNMILDDGGDLTNLIHTKYPOLLPGIRGISETTTGVHNLKYMANGILKVPAINVND 184
Db 126 LNMILDDGGDLTNLIHTKYPOLLPGIRGISETTTGVHNLKYMANGILKVPAINVND 185
QY 185 TSKEFDNLYGCRSLIDGIRKATDVMIAGKAVVAGYGVGKCAQALRGFGARVIIT 244
Db 186 TSKEFDNLYGCRSLIDGIRKATDVMIAGKAVVAGYGVGKCAQALRGFGARVIIT 245
QY 245 DPINALQAAMEGYEVTMTDEACQEGNIFVTTTGCIDIIILGRHFEQMKDDAIVCNIGHF 304
Db 246 DPINALQAAMEGYEVTMTDEAAVKEQIFVTTTGCIDIIIRGEHFNEMKEDSIVCNIGHF 305
QY 305 EIDVKWLNENAVEKNIKQVDYRLKNGRRILLAEGRVLNLCAMGHPSPFVMSNSF 364
Db 306 EIDVAWLKANAKADVNIKQVDYRLKNGRRILLAEGRVLNLCAMGHPSPFVMSNSF 365
QY 365 QVMAQIELWTHDPKYPVGVHFLPKKLDEAVAHAHLGKLNVLTKLTEKQAQYLGMS 424
Db 366 QVLAQIALWTDNTSYPLGVHMLPKKLDEAVAHAHLGKLNVLTKLTTSVQSDYLGIVDGP 425

RESULT 4
US-10-369-493-2430
; Sequence 2430, Application US/10369493

; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1740
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae

US-10-369-493-1740

Query Match 71.9%; Score 1633; DB 12; Length 449;
Best Local Similarity 70.8%; Pred. No. 3.7e-156;
Matches 313; Conservative 52; Mismatches 61; Indels 16; Gaps 3;

DY 7 YKVDATGLAANGRKALDIAENEMFGLMRMRRYSASKPLKGARIAGCLHMTVETAVLIET 66
|||:::||||:::|||:::||||:::|||:::||||:::|||:::||||
Db 8 YKIADISLAAPGRKEIELABHEMFGLMAIRKAYGVQPLKGARIAGCLHMTIQTAVLIET 67
|||:::||||:::|||:::||||:::|||:::||||:::|||:::||||
DY 67 LVTLGARVOWSSNCNIFSTONHAARAAIKAGIPVVAWKGETDBEYLWCIETQLY-PKDGP-P 124
|||:::||||:::|||:::||||:::|||:::||||:::|||:::||||
Db 68 LVALGAEVTWSSCNINYSTDQHAAAIIAASGVVPFAWKGETBEEYLWCIEQQLPAFKDNKK 127
|||:::||||:::|||:::||||:::|||:::||||:::|||:::||||
DY 125 LNMLDDGGDLTNLHKYPOLLPFGIRGISSETTTGVHNLYKMAMNGILKVPAINVDSV 184
|||:::||||:::|||:::||||:::|||:::||||:::|||:::||||
Db 128 LNLILLDDGGDLTLLVEKHPEMLEDCFLSSEITTVGHVHYRMVKEGKLKVPAINVDSV 187
|||:::||||:::|||:::||||:::|||:::||||:::|||:::||||
DY 185 TKSFDNLYCRESLIDIGIKRATDMVIAGKVVAHVAGYGDVGKCAOALRGFGARVIIITEI 244
|||:::||||:::|||:::||||:::|||:::||||:::|||:::||||
Db 188 TKSFDNLYCRESLVBDGIKRATDMVLAKGVAVVAGYGDVGKCAALRGGMARGARVLVTEI 247
|||:::||||:::|||:::||||:::|||:::||||~::~:
DY 245 DPINALQAAMEGYEVTTMDACQSGNFVTTTGCTDIITLGHRHFPMOKDAIVCNIGHFDV 304
|||:::||||:::|||:::||||:::|||:::||||:::|||:::||||
Db 248 DPINALQAAMEGYQVWTMEDASHYGQPVPTTTCRDIIINGEHFINNPEDAIVCNIGHFDI 307
|||:::||||:::|||:::||||:::|||:::||||~::~:
DY 305 EIDVMKNLENAVEKNVTKPOVDRLXGNRIILLAEGRVLNLGCAMGHPSFMWSNSTN 364
|||:::||||:::|||:::||||~::~:
Db 308 EIDVAMLKANAKECINIKPQVDRYLLSGRHVILLANGLRVNLGCATGHSSPFWSCSPSN 367
|||:::||||~::~:
DY 365 QVNMAQIELWTHPDK-----YPGVNHFPKKLDDEAVAHAHLKLNVLTKLT 410
|||:::||||~::~:
Db 368 QVLAQIALFKSNDKSPREKHIEFOKTGFPEVGVHVLPKILDGAFAKHLGNLGRUTKLS 427
|||:::||||~::~:
DY 411 EKQAOYLGMSCDGPPKDPDHRY 432
:||||:||||~::~:
Db 428 KVQSEYLGIPEGPFKADHRY 449
|||:::||||~::~:

RESULT 6
US-10-369-493-3683
; Sequence 3683, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3683
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Neurospora crassa

US-10-369-493-3683

Query Match 70.2%; Score 1594; DB 12; Length 447;
Best Local Similarity 69.8%; Pred. No. 3.2e-152;
Matches 307; Conservative 52; Mismatches 65; Indels 16; Gaps 3;

Qy	7	YKVADIGLAAMGRKALDIAENEMPGLMRMRRYSASKPLKGARIAGCLHMTVTAVLIET	66
Db	8	FKVADLSLAAFGRKEIEIAENEMPGLMATRKYYAADQPLKGARIAGCLHMTIQTAVLIET	67
Qy	67	LVTLGAEVOWSSCNIFSTONIAAAAAIAKAGIPVYAWKGETDEEYLCWICEOTLA-FKDG-P	124
Db	68	LTALGAEVWTSSCNIFSQDHAHAIAAAGVPVFAWKGETEEYQWCEOQLTAFKDNKK	127
Qy	125	LNMLDDGGDLTNLIHTKYPOLLPGIRGISEBTTTGVHNLKMMANGILKVPAINVNSDV	184
Db	128	LNMLDDGGDLTHLVHTKYPKEMLEDCFGVSEBTTTGVHLYRMLKEGKLLVPAINVNSDV	187
Qy	185	TKSKFDNLYGCRESLIDGIKRATDMVIAGVAVVAGYGDVYGKCAQALRGFGARVITETI	244
Db	189	TKSKFDNLYGCRESLVDGIKRATDMVIAGKIAVVAGFGDVGKGCAMALSGMARVITVEV	247
Qy	245	DPINALQAAMBEYEVTTTMDCAQCBGNIFVTTTGCIDIIILGRHPEQMKDDAIVCNIGHFDV	304
Db	248	DPINALQAAMAGYQVTTTWEKAAPLGQIFVTTTGCIRDILVGKHFVEMDAILVCNIGHFDV	307
Qy	305	EIDVQWLHNAVEKVNIIKPOQVDRVRLKNGRRIILLAEGRLVNLGCAMGHSFVMSNFTN	364
Db	308	EIDVAWLKANAASVQNIKPOQVDRFLMKNGRRIILLAEGRLVNLGCATGSHSSFVMSCFN	367
Qy	365	QVMAQIELWTHPD-----KYPGVGHFLPKKLDEAAEAHLGKLVKLTKL	410
Db	368	QVLAQIMLYKANDEAFSNKYVEFGSKGLEKKVTVLPKILDEEVARLHLDHCNVELTQLS	427
Qy	411	EKQAOYLGMSCDGPPKPDHY	430
Db	428	DVQAEYVLGATEGPYKSDQY	447

RESULT 7

```

US-10-369-493-10135
; Sequence 10135, Application US/10369493
; Publication NO. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 10135
; LENGTH: 426
; TYPE: PRT
; ORGANISM: magnetite-containing magnetic coccus
US-10-369-493-10135

```

185	Qy	TKSKFDNLYGCRSLIDGIKATDVMIAAGVAVVAGYGDVGKCAQALRGFGGARVITTEI	244
186		: : : : : : : : : : :	
187		: : : : : : : : : :	
188		: : : : : : : : : :	
189		: : : : : : : : : :	
190		: : : : : : : : : :	
191	Db	TKSKFDNLYGCRSLMDGIIKATDVMIAAGIIVGVCGYGDVGKCAQAFRLGAVVWVTEI	240
192		: : : : : : : : : :	
193		: : : : : : : : : :	
194		: : : : : : : : : :	
195		: : : : : : : : : :	
196		: : : : : : : : : :	
197		: : : : : : : : : :	
198		: : : : : : : : : :	
199		: : : : : : : : : :	
200		: : : : : : : : : :	
201	Qy	DPINALQAAMGEYVVTWDEACQSGNIFVTTTCGIDIIILGRHFEQMKDDAIVCNIGHFDV	304
202		: : : : : : : : : :	
203		: : : : : : : : : :	
204		: : : : : : : : : :	
205		: : : : : : : : : :	
206		: : : : : : : : : :	
207	Db	DPICALQAAMGYYVVTWEEEAASQDIFVTATGNRDIITRAHFEQMKDQDAIVCNIGHFDS	300
208		: : : : : : : : : :	
209		: : : : : : : : : :	
210		: : : : : : : : : :	
211		: : : : : : : : : :	
212		: : : : : : : : : :	
213		: : : : : : : : : :	
214		: : : : : : : : : :	
215		: : : : : : : : : :	
216		: : : : : : : : : :	
217		: : : : : : : : : :	
218		: : : : : : : : : :	
219		: : : : : : : : : :	
220		: : : : : : : : : :	
221	Qy	EIDVKWLNENAVEKVINQPDVRYLKNGRRIILLAEGRLVNLGCAMGHPSFVMSNFTN	364
222		: : : : : : : : : :	
223		: : : : : : : : : :	
224		: : : : : : : : : :	
225		: : : : : : : : : :	
226		: : : : : : : : : :	
227	Db	EIDIASIRE--LKWDNIKPDVDHVTMPSGNRRIIVLAEGRLVNLGCATGHPSFVMSNFTN	358
228		: : : : : : : : : :	
229		: : : : : : : : : :	
230		: : : : : : : : : :	
231		: : : : : : : : : :	
232		: : : : : : : : : :	
233		: : : : : : : : : :	
234		: : : : : : : : : :	
235	Qy	QYMAQIELWTHPDXYVPGVHPLPKLDEAVAEAHGLKLVNKLTKLTKAQAYLGMSCDGP	424
236		: : : : : : : : : :	
237		: : : : : : : : : :	
238		: : : : : : : : : :	
239	Db	QYMAQIELFNRGEMTENRVYVPLKHLDEKVARLHLAKVGAKLTTLTQVQADYLGISVDGP	418
240		: : : : : : : : : :	
241		: : : : : : : : : :	
242		: : : : : : : : : :	
243		: : : : : : : : : :	
244	Qy	KFPDHYR	432
245		:	
246			
247	Db	YKSDHYR	426
248			

RESIST 8

```

US-10-369-493-13111
; Sequence 13111, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13111
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(516)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-13111

```

	Query Match	68.1%	Score 1546;	DB 12;	Length 426;
	Best Local Similarity	69.9%;	Pred. No. 2.1e-147;		
	Matches 299;	Conservative 47;	Mismatches 78;	Indels 4;	Gaps 3
QY	7	YKVADIGLAANGRKALDIAENMPLMRERYSASKPLKGARIACIILHMTVETAVLTET	66		
Db	1	PKVADIGLAANGRKKEIETAEETMPLVSLRSEYSGAQPLKGARVACGLHMTTQTAVLTET	60		
QY	67	LVTLCGEYQWSSCNIFSTQNHAAAAIAKAGIPVYANKGETDEBYLWCIEQTLVFKDGPL-	125		
Db	61	LTALCGEYRWSNCNIFSTQDHAHAHAIAAAGVPFANKGETSEYVWCVEQTITKGDGWPV	120		
QY	126	NMLDDGDGLTNLIH-TKYPQLPFGIRGISEETTTGVHNLVKMANGIILKVPAINVNSV	184		
Db	121	NMLDDGDGLTEILHRPEYVEIMKVRGISEETTTGVLYRMAOKGLECAEFNNVNSV	180		

Query Match	64.5%;	Score 1465;	DB 12;	Length 428;
Best Local Similarity	66.2%;	Pred. No. 3.36-139;		
Matches	284;	Conservative 58;	Mismatches 83;	Indels 4; Gaps 3;
Qy	7	YKVADIGLAAGKALDIAENEMPLMRMBERYSASKPLKGCARTAGCGLHMTVETAVLIET	66	
Db	1	HKVADISLAAGRKELISLAAGMPLGMSIRKEFGPSKPLGARVAGCGLHMTIQIYAVLIET	60	
Qy	67	LVTLGAEVOMSSCNIFSTQNHAAAAIAKAGIPVYAWKGETDEEYLCWICEQTLYFKDG--P	124	
Db	61	LIELGAETVWSSCNIFSTQDHAAAAIAAAGISVYAWKGMNEEFPDWCIEQTLFFGEDRKP	120	
Qy	125	LNMLIDGGDLTNLIHTKYQLLPGLPIRGISEETTTGVHNLKYMANGILKVPAINVDSV	184	
Db	121	LNMLIDGGDLTNMLVDFPDLVKDIRGISEETTTGVLRLKDRERNSGLVLPAINVDSV	180	
Qy	185	TKSKFDNLYGCRSLIDGIKRATDMITAGKVAVVAGVDYGVKGCQAQLRFGGARVITETI	244	
Db	181	TKSKFDNKYCKESLVDISIRRAITDVMAGKVAVVAGYGVKGSAAISLRGAGARVITETI	240	
Qy	245	DPINALQAAMEGYEVTMTDEACQEGNIFVTTTGCIDIILGBHFQMKDDAIVCNIGHFDV	304	
Db	241	DPICALQAAMDGEVKKVADAVKRAIDVVTATGNKNIITGEHFKAMRDKIVCNIGHFDN	300	
Qy	305	EIDVKNLLEN--AVBKVNKIKPOVDYRLKNGRRRIILLAEGRVLNVLGCAMGHPSPFVMSNFT	363	
Db	301	EIDMAWLNKTYGSTKVTYKQVDIYNV-DGHDVILLAEGRVLNVLGCATGHPSPFVMSNFS	359	
Qy	364	NOVMAQIELMTHDPKYPVGVHFIPLKKLDEAVAEAHGLKLNVLTKLTKEQAYQLGMSCDG	423	
Db	360	NOVIAQELMENSRYENKYVITLPKSLDEKVARLHLSKIDVELDILSADQAAAYIGTVVDG	419	

Query Match	62.9%	Score 1428	DB 12	Length 468
Best Local Similarity	61.3%	Pred. No. 2.le-135		
Matches 287	Conservative 52	Mismatches 87	Indels 42	Gaps 6
Qy 7	YKVADTGLAANGRKALDIAENHPGLMRPRYSASKPLKGARIAGCLHMTVAVLIET	66		
Db 1	YKDIADISLADWGRKEIDIAEHENPGLMSIRRVASKQPLKGRVTVGSLHMTIQTVAVLIET	60		
Qy 67	LVTLGAEVONSSCNIFSTQNHAAATAKAGIPVYAWKGETDBEYLWCIEOTLYP--KDG 124			
Db 61	LKDIGADVWRVASCNIFSTQDHAAATAATSGTPVFWKGETLEBYDWDCTLQALITFLADGT	120		
Qy 125	L---NMILDDGGDLTNLIHTKY-----PQLL-----PGI--- 150			
Db 121	LTPGELLVDDGGDATLLIHKGYELENGSTWVDPSSDLEBOVKRLKRLKRIARPPGYWTR	180		
Qy 151	-----RGISBETTTGVHNLVYKMANGILKYPAINVNDSTVTKSPFDNLYGCRESLIIDGIR	205		
Db 181	VNDWKVGSBETTTGVHRLYQIAATGRLLVPAINVNDSTVTKSPFDNLYGCRESLADGLKR	240		
Qy 206	ATDVMTAGVAVVAGYGDVCKGCAQALRGFGARVITEIDPINALQAAHGEYVTTWDEA	265		
Db 241	AMDVMLAGLAVVCGYGDVGKSAHSLRAYGARVIVTEIDPICALQAAHGEFVTTVEDT	300		
Qy 266	CQSGNIFVTTTGCDIILGLHFQOMKDDATVCNIGHDFDVIDVKWLN--NAVEKVNKKPQ	324		
Db 301	LQGADIYVTTTGKQDVIRIEHMTAMKQDVIVCNIGHDFDNEIQVDALNTLTCGVQKINIKPQ	360		
Qy 325	VDRYRLKNGRRRIILLAEGRVLNLCGAMGHPSPVMSNSFTTNVMAQIELMTHPPDKYPVGVH	384		
Db 361	VDFKILPNGNTLFLAEGRLVNLGCATGHPSPVMSNSFANQTLAQIDLQNKQDVYKGVY	420		
Qy 385	FLPKLDEAAVAEHLGKLVNKLTKLTEKQAYQLGMSCDGPFKPDHYRY	432		
Db 421	RLPKLDEEVARLHLEKIGVKLTTLTANQAYLGISVEGPFKEPHRY	468		

RESULT 11
US-10-369-493-9386
; Sequence 9386, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 9386
LENGTH: 468
TYPE: PRT
ORGANISM: Xylella fastidiosa
US-10-369-493-9386

Query Match 62.6%; Score 1422; DB 12; Length 468;
Best Local Similarity 61.1%; Pred. No. 8.6e-135;
Matches 286; Conservative 52; Mismatches 88; Indels 42; Gaps 6;

QY 7 YKVDIGLAAGWKALDIAENEMPGMLMRMRYSASKPLKGARIAGCLHMTVETAVLIET 66
DB 1 YKIADISLADWGRKEIDIAEHMPLGMSIRRYKVASQPLKGVVVTGSLHMTIQTAVLIET 60
QY 67 LVTLGAEVQWSSCNIFSTQNHAAAAIAKAGIPYVANKGETDEEYLWCIEQTLYF--KQGP 124
DB 61 LXDIGADVWASCNIFSTQDHAAAAIATSGTPVFAWKGETLEEYWDCTIQAULTFTLADGT 120
QY 125 L---NMILDDGGDLTLNHTKY-----POLL-----PGI--- 150
DB 121 LTPGLIVDDGGDATTLLHKGYELENGSTWDEPSLSSEQVTKRLKLLKIAIERPGYWR 180
QY 151 -----RGISETTGVNHYLYKMMANGILKVPAINVNDSTVTKSFDNLYGCRSLIDGKR 205
DB 181 VVNDWKGSEETTTGVHRLYQIAATGRLLVPAINVNDSTVTKSFDNLYGCRSLADGLKR 240
QY 206 ATDVMTAGVAVVAGVGVGKCAQALRGFGARVITTEIDPINALQAAMEGVEVTTMDRA 265
DB 241 AMDVMTAGVAVVAGVGVGKCAQALRGFGARVITTEIDPINALQAAMEGVEVTTMDRA 300
QY 266 COEGNIFVTTTGCIDIIILGRHFQMKDDAIVCNIGHFQVEIDVKWLINE-NAVEKVNKIQ 324
DB 301 LGQADIVTTTGNKQVIRIEHTMTAMKQDVIVCNIGHFQVEIDVKWLINE-NAVEKVNKIQ 360
QY 325 VDRYLKNGRRRIILLAEGRVLNLCAMGHPSPFVMSNSTNQVMAQIELMTHPDKYPVGVH 384
DB 361 VDKFILPNGNTLLAEGRVLNLCAMGHPSPFVMSNSTNQVMAQIELMTHPDKYPVGVH 420
QY 385 FLPKLDEAVAEHLKLNKLVTKLTKTEKQAQYLGMSCDGPFKPDHYRY 432
DB 421 RUPKGLDEEVARLHLEKIGVKTLLTANQAAYLGISVEGPFKPDHYRY 468

RESULT 12
US-10-369-493-8266
Sequence 8266, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 8266
LENGTH: 476
TYPE: PRT
ORGANISM: Thermobifida fusca
US-10-369-493-8266

Query Match 61.9%; Score 1406; DB 12; Length 476;
Best Local Similarity 58.9%; Pred. No. 3.7e-133;
Matches 279; Conservative 57; Mismatches 90; Indels 48; Gaps 4;

QY 7 YKVDIGLAAGWKALDIAENEMPGMLMRMRYSASKPLKGARIAGCLHMTVETAVLIET 66
DB 3 FKVADLSLAEPGKKEIRLAHEMPLGMASTRASFGPKPLRGAKITGSLHMTVETAVLIET 62
QY 67 LVTLGAEVQWSSCNIFSTQNHAAAAIA-----KAGIPYVANKGETDEEYLWCIEQT 117
DB 63 LVELGAEVWASCNIFSTQDHAAAAAVVVGPDGTPDNPRGVPVFAWKGETLEEYWMCTEQ 122
QY 118 LYFKDGP-LNMILDDGGDLTLNLIH----- 140
DB 123 LTPGEGENMILDDGGDATMLVHKGVQYKAGAVDPDPTADSEPRIVLELLRRTLAEN 182
QY 141 -TKYPQLLPGIRIGISETTGVNHYLYKMMANGILKVPAINVNDSTVTKSFDNLYGCRSL 199
DB 183 PRKWTIASRIKGVTEETTTGVHRLYEMQSGTLLFPAINVNDSTVTKSFDNLYGCRSL 242
QY 200 IDGIRATDVMTAGVAVVAGVGVGKCAQALRGFGARVITTEIDPINALQAAMEGVEV 259
DB 243 IDGIRATDVMTAGVAVVAGVGVGKCAQALRGFGARVITTEIDPINALQAAMEGVEV 302
QY 260 TTMDEACQEGNIFVTTTGCIDIIILGRHFQMKDDAIVCNIGHFQVEIDVKWLINE-NAVEK 318
DB 303 TTLDEWETADIFITATGNRDVITAEHMAKQQAIVGNIGHFQVEIDWAGLAAPGIBK 362
QY 319 VNKPQVDRYLKNGRRRIILLAEGRVLNLCAMGHPSPFVMSNSTNQVMAQIELMTHPDK 378
DB 363 IEIKPQVHWRPDPGHSIIVLSEGRLLNLTGNATGHPSPFVMSNSTNQVMAQIELMTHPDK 422
QY 379 YPVGHFLPKLDEAVAEHLKLNKLVTKLTKTEKQAQYLGMSCDGPFKPDHYRY 432
DB 423 YPTGVVLPFKHLEKIGVKTLLTANQAAYLGISVEGPFKPDHYRY 476

RESULT 13
US-10-369-493-8750
Sequence 8750, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 8750
LENGTH: 466
TYPE: PRT
ORGANISM: Ralstonia metallidurans
US-10-369-493-8750

Query Match 61.9%; Score 1405; DB 12; Length 466;
Best Local Similarity 60.9%; Pred. No. 4.5e-133;
Matches 287; Conservative 53; Mismatches 83; Indels 48; Gaps 7;

QY 4 KLPYKVDIGLAAGWKALDIAENEMPGMLMRMRYSASKPLKGARIAGCLHMTVETAVL 63

Db 2 KQDYIVADIGLAGWGRKEIAIAETEMPGMLMAIRDEFAPAAQPLKGARIAGSLHMTIQTAVL 61
QY 64 IETVLTLGAEVQWSSCNIFSTONHAAAAIAKAGIPVYAWKGETDEBYLWCIEQTLV-FKD 122
Db 62 IETLKALGADVWASCNIFSTQDHAHAATAASGTPVAFKGSLSKEY-WDFTHRIFDWD 120
QY 123 GPL-NMILDDGGDLTLNLIH-----TKYPOL 146
Db 121 GGTNNMILDDGGDATALLLHLGARAEDASLIAKPTSEETFLFAAIEKELAKDSTWYSRN 180
QY 147 LQIRGISSETTTGVHNLKYMANGILKVPAINVNDVTSKSPDNLYGCRSLIDGICKA 206
Db 181 LAAIRGVTEETTTGVHRLYQMAQKGLKFPAINVNDVTSKSPDNLYGCRSLVDGICKA 240
QY 207 TDVMIAGKAVVAGYGVGVGKGAQALRGFARVITTEIDPINALQAAMEGYEVTWDEAC 266
Db 241 TDVMIAGKAVVAGYGVGVGKGAQALRALSAQVWTEIDPICALQAAMEGYRVWTDYAA 300
QY 267 QEGNIFVTTTCIDIIILGRHFEQMKDDAIVCNIGHFDEVIDVKMLNENAVEKV---NIK 323
Db 301 EHGDIPTCTGNVHTHDMAMKQDAIVCNIGHFDEVIDIA-----SVEKYEWDEIKP 355
QY 324 QVDYRLKNGRRRIILLAGRLVNLGCAMGHPSPVMSNSTNQVMAQIELWTHPD--KYPV 381
Db 356 QVDHVRFPDPKKIILAKRLVNLGCATGHPSPVMSNSTNQVMAQIELWTHPD--KYPV 415
QY 382 GVHFLPKLDEAAVAEHLGKLVNKLTKLTKAQOAYLGMSCDGPFPKPDHYRY 432
Db 416 GVTVLPKHLDEKVARLQRLKLNALQELTEQQAAYIGVKEGYPKADHYRY 466

RESULT 14
US-10-369-493-15745
; Sequence 15745, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 15745
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Xanthomonas campestris
US-10-369-493-15745

Query Match 61.7%; Score 1401; DB 12; Length 469;
Best Local Similarity 60.9%; Pred. No. 1.1e-132;
Matches 285; Conservative 45; Mismatches 96; Indels 42; Gaps 6;

QY 7 YKVADIGLAAGWKALDIAENMPGLMRERYASASKPLKGARIAGCLHMTVETAVLIET 66
Db 2 YKIADISLADWGRKELDIAEHMPGLMSIRKHAQTKPLKDVRIITGSLHMTIQTAVLIET 61
QY 67 LVTLGAEVQWSSCNIFSTONHAAAAIAKAGIPVYAWKGETDEBYLWCIEQTLV-FKDGP 124
Db 62 LKDIGANVRWASCNIFSTQDHAHAATAASGTPVFAWKGETLEBYWDCDTLDTLTPDGT 121
QY 125 L---NMILDDGGDLTLNLIHKT-----PGL--- 150
Db 122 LTGPELVDDGGDVTLLIHKGYLENGSTWVDEPASPHEEGVIALKRVAVERPQYWAR 181
QY 151 -----RGISEETTTGVHNLKYMANGILKVPAINVNDVTSKSPDNLYGCRSLIDGICKR 205
Db 2 YKIADISLADWGRKELDIAEHMPGLMSIRKHAQTKPLKDVRIITGSLHMTIQTAVLIET 61
QY 67 LVTLGAEVQWSSCNIFSTONHAAAAIAKAGIPVYAWKGETDEBYLWCIEQTLV-FKDGP 124
Db 62 LKDIGANVRWASCNIFSTQDHAHAATAASGTPVFAWKGETLEBYWDCDTLDTLTPDGT 121
QY 125 L---NMILDDGGDLTLNLIHKT-----PGL--- 150
Db 122 LTGPELVDDGGDVTLLIHKGYLENGSTWVDEPASPHEEGVIALKRVAVERPQYWAR 181
QY 151 -----RGISEETTTGVHNLKYMANGILKVPAINVNDVTSKSPDNLYGCRSLIDGICKR 205

Db 2 YKIADISLADWGRKELDIAEHMPGLMSIRKHAQTKPLKDVRIITGSLHMTIQTAVLIET 61
QY 67 LVTLGAEVQWSSCNIFSTONHAAAAIAKAGIPVYAWKGETDEBYLWCIEQTLV-FKDGP 124
Db 62 LKDIGANVRWASCNIFSTQDHAHAATAASGTPVFAWKGETLEBYWDCDTLDTLTPDGT 121
QY 125 L---NMILDDGGDLTLNLIHKT-----PGL--- 150
Db 122 LTGPELVDDGGDVTLLIHKGYLENGSTWVDEPASPHEEGVIALKRVAVERPQYWAR 181
QY 151 -----RGISEETTTGVHNLKYMANGILKVPAINVNDVTSKSPDNLYGCRSLIDGICKR 205

Db 182 VVKDWKGVSEETTTGVHRLYQIAEAGKLLIPAINVNDVTSKSPDNLYGCRSLADGLKR 241
QY 206 ATDVMIAGKAVVAGYGVGVGKGAQALRGFARVITTEIDPINALQAAMEGYEVTWMDKA 265
Db 242 AMDVNLAKVAVVCGYGVGVGKGAASLRAYGARVITTEIDPICALQAASMEGEVNTIEST 301
QY 266 COEGNIFVTTTCIDIIILGRHFEQMKDDAIVCNIGHFDEVIDVKWLNE-NAVEKVNIKPQ 324
Db 302 LGRGDIYVTTTGNKDIITVEHLQAMKQDAIVCNIGHFONEIQVDALNALKGVEKINIKPQ 361
QY 335 VDRYRLKNGRRRIILLAGRLVNLGCAMGHPSPVMSNSTNQVMAQIELWTHPDKYPVGVH 384
Db 362 VDKYVFGNGAIFLLADGRLVNLGCATGHPSPVMSNSTNQVMAQIELWTHPDKYPVGVH 421
QY 385 FUPKKLDEAAVAEHLGKLVNKLTKLTKAQOAYLGMSCDGPFPKPDHYRY 432
Db 422 ILPKHLDEAVARLHLEKIGVKLTITLKQADYLVGVVAGPYKPDHYRY 469

RESULT 15
US-10-369-493-16129
; Sequence 16129, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16129
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Xanthomonas campestris
US-10-369-493-16129

Query Match 61.7%; Score 1401; DB 12; Length 469;
Best Local Similarity 60.9%; Pred. No. 1.1e-132;
Matches 285; Conservative 45; Mismatches 96; Indels 42; Gaps 6;

QY 7 YKVADIGLAAGWKALDIAENMPGLMRERYASASKPLKGARIAGCLHMTVETAVLIET 66
Db 2 YKIADISLADWGRKELDIAEHMPGLMSIRKHAQTKPLKDVRIITGSLHMTIQTAVLIET 61
QY 67 LVTLGAEVQWSSCNIFSTONHAAAAIAKAGIPVYAWKGETDEBYLWCIEQTLV-FKDGP 124
Db 62 LKDIGANVRWASCNIFSTQDHAHAATAASGTPVFAWKGETLEBYWDCDTLDTLTPDGT 121
QY 125 L---NMILDDGGDLTLNLIHKT-----PGL--- 150
Db 122 LTGPELVDDGGDVTLLIHKGYLENGSTWVDEPASPHEEGVIALKRVAVERPQYWAR 181
QY 151 -----RGISEETTTGVHNLKYMANGILKVPAINVNDVTSKSPDNLYGCRSLIDGICKR 205
Db 182 VVKDWKGVSEETTTGVHRLYQIAEAGKLLIPAINVNDVTSKSPDNLYGCRSLADGLKR 241
QY 206 ATDVMIAGKAVVAGYGVGVGKGAQALRGFARVITTEIDPINALQAAMEGYEVTWMDKA 265
Db 242 AMDVNLAKVAVVCGYGVGVGKGAASLRAYGARVITTEIDPICALQAASMEGEVNTIEST 301
QY 266 COEGNIFVTTTCIDIIILGRHFEQMKDDAIVCNIGHFDEVIDVKWLNE-NAVEKVNIKPQ 324
Db 302 LGRGDIYVTTTGNKDIITVEHLQAMKQDAIVCNIGHFONEIQVDALNALKGVEKINIKPQ 361
QY 335 VDRYRLKNGRRRIILLAGRLVNLGCAMGHPSPVMSNSTNQVMAQIELWTHPDKYPVGVH 384
Db 362 VDKYVFGNGAIFLLADGRLVNLGCATGHPSPVMSNSTNQVMAQIELWTHPDKYPVGVH 421
QY 385 FUPKKLDEAAVAEHLGKLVNKLTKLTKAQOAYLGMSCDGPFPKPDHYRY 432
Db 422 ILPKHLDEAVARLHLEKIGVKLTITLKQADYLVGVVAGPYKPDHYRY 469

Db 362 VDKYVFGNGNAIFLLADGRLVNLGCATGHPSPVMSNSFANQTLAQIDLMEKRDSEYKQVY 421
Qy 385 FLEPKLDEAVAEAHLGKLVKLTKLTQKQAYLGMSCDGPFKDPHYRY 432
Db 422 ILPKHLDDEVARLHLEKIGVKLTTLTKQADYLGVDVAGEYKDPHYRY 469

Search completed: December 30, 2003, 10:47:06
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:39:38 ; Search time 21 Seconds
(without alignments)
870.395 Million cell updates/sec

Title: US-10-043-787-1

Perfect score: 2271
Sequence: 1 MSDKLPYKVADIGLAAMGRK.....QAQLGMSCDGPKPDHYRY 432

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2271	100.0	432	2	US-08-896-005-4
2	2271	100.0	432	4	US-09-347-878-1
3	2193	96.6	432	2	US-08-896-005-5
4	1289	56.8	485	3	US-08-930-894-2
5	1249.5	55.0	502	4	US-09-252-991A-23501
6	1222	53.8	463	4	US-09-328-352-4600
7	1149.5	50.6	504	2	US-08-896-005-3
8	1146	50.5	500	2	US-08-896-005-1
9	421	18.5	97	1	US-08-204-740-7
10	421	18.5	97	3	US-09-081-167A-7
11	421	18.5	97	3	US-09-081-395-7
12	421	18.5	97	3	US-09-416-833-7
13	421	18.5	97	5	PCT-US95-02521-7
14	388	17.1	95	1	US-08-204-740-9
15	388	17.1	95	3	US-09-081-167A-9
16	388	17.1	95	3	US-09-081-395-9
17	388	17.1	95	3	US-09-416-833-9
18	388	17.1	95	5	PCT-US95-02521-9
19	347	15.3	99	3	US-08-930-894-8
20	249.5	11.0	138	3	US-08-930-894-5
21	229.5	10.1	140	3	US-08-930-894-4
22	228	10.0	139	3	US-08-930-894-7
23	224	9.9	139	3	US-08-930-894-6
24	112.5	5.0	485	4	US-09-252-991A-25242
25	103.5	4.6	257	4	US-09-134-001C-3562
26	98.5	4.3	683	4	US-09-816-093-2
27	98	4.3	449	4	US-09-530-836-2

28	98	4.3	1302	1	US-08-232-537-2	Sequence 2, Appli
29	97.5	4.3	461	4	US-09-134-001C-3892	Sequence 3892, Ap
30	97.5	4.3	539	4	US-09-134-001C-5118	Sequence 5118, Ap
31	96.5	4.2	1261	3	US-09-080-855-2	Sequence 2, Appli
32	96.5	4.2	1261	4	US-09-566-076-2	Sequence 2, Appli
33	95.5	4.2	349	4	US-09-134-001C-4884	Sequence 4884, Ap
34	93.5	4.1	345	3	US-09-222-817-2	Sequence 2, Appli
35	93.5	4.1	345	3	US-09-222-786-2	Sequence 2, Appli
36	93.5	4.1	530	3	US-09-222-817-12	Sequence 12, Appli
37	93.5	4.1	530	3	US-09-222-817-14	Sequence 14, Appli
38	93.5	4.1	530	3	US-09-222-786-12	Sequence 12, Appli
39	93.5	4.1	530	3	US-09-222-786-14	Sequence 14, Appli
40	93	4.1	480	4	US-09-252-991A-28668	Sequence 28668, A
41	92	4.1	586	4	US-09-134-001C-4456	Sequence 4456, Ap
42	92	4.1	1297	4	US-09-328-352-6373	Sequence 6373, Ap
43	91	4.0	546	3	US-08-470-260-6	Sequence 6, Appli
44	91	4.0	546	3	US-08-471-491-6	Sequence 6, Appli
45	91	4.0	546	3	US-08-466-662-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-896-005-4
; Sequence 4, Application US/08896005
; Patent No. 5854023
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,005
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0337 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 178277
; US-08-896-005-4

Query Match 100.0%; Score 2271; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.2e-246;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDKLPYKVDIGLAAGWKALDIAENEMPGMLMRERYASGSKPLKGARIAGCLHMTVET 60
DB 1 MSDKLPYKVDIGLAAGWKALDIAENEMPGMLMRERYASGSKPLKGARIAGCLHMTVET 60
QY 61 AVLIETLVTLAGAEVQWSSCNIFSTONHAAIAIAKAGIPVYAWKGETDEEYLWCIEQTLF 120
DB 61 AVLIETLVTLAGAEVQWSSCNIFSTONHAAIAIAKAGIPVYAWKGETDEEYLWCIEQTLF 120
QY 121 KDGPLNMLDDGGDLTNLIHTKYPQLLPGIRGISEETTTGVHNLKWMANGILKVPAINV 180
DB 121 KDGPLNMLDDGGDLTNLIHTKYPQLLPGIRGISEETTTGVHNLKWMANGILKVPAINV 180
QY 181 NDSVTSKFDNLGCRSLIDGIKRATDVMTAGVAVVAGYGVGKGCACALRGFGARVI 240
DB 181 NDSVTSKFDNLGCRSLIDGIKRATDVMTAGVAVVAGYGVGKGCACALRGFGARVI 240
QY 241 ITEIDPINALQAAMEGYEVTTMDEACQEGNIFVTTTGCIDIIILGRHFEQMKDDAIVCNIG 300
DB 241 ITEIDPINALQAAMEGYEVTTMDEACQEGNIFVTTTGCIDIIILGRHFEQMKDDAIVCNIG 300
QY 301 HFDVEIDVKWLNENAVEKVNIPQVDYRLKNGRRRIILAEGRVLNLCGAMGHPSPFVMSN 360
DB 301 HFDVEIDVKWLNENAVEKVNIPQVDYRLKNGRRRIILAEGRVLNLCGAMGHPSPFVMSN 360
QY 361 SFTNQVMAQIELTHDPKYPVGVHFLPKLDEAVABHLGKLVNKLTKLTEKQAOYLGM 420
DB 361 SFTNQVMAQIELTHDPKYPVGVHFLPKLDEAVABHLGKLVNKLTKLTEKQAOYLGM 420
QY 421 CDGPFKPDHYRY 432
DB 421 CDGPFKPDHYRY 432

RESULT 2

US-09-347-878-1
; Sequence 1, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25885-1651
; CURRENT APPLICATION NUMBER: US/09/347,878C
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human S-adenosylhomocysteine hydrolase protein
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: M61831/GenBank
US-09-347-878-1

Query Match 100.0%; Score 2271; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.2e-246;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDKLPYKVDIGLAAGWKALDIAENEMPGMLMRERYASGSKPLKGARIAGCLHMTVET 60
DB 1 MSDKLPYKVDIGLAAGWKALDIAENEMPGMLMRERYASGSKPLKGARIAGCLHMTVET 60
QY 61 AVLIETLVTLAGAEVQWSSCNIFSTONHAAIAIAKAGIPVYAWKGETDEEYLWCIEQTLF 120
DB 61 AVLIETLVTLAGAEVQWSSCNIFSTONHAAIAIAKAGIPVYAWKGETDEEYLWCIEQTLF 120
QY 121 KDGPLNMLDDGGDLTNLIHTKYPQLLPGIRGISEETTTGVHNLKWMANGILKVPAINV 180
DB 121 KDGPLNMLDDGGDLTNLIHTKYPQLLPGIRGISEETTTGVHNLKWMANGILKVPAINV 180

QY 181 NDSVTSKFDNLGCRSLIDGIKRATDVMTAGVAVVAGYGVGKGCACALRGFGARVI 240
DB 181 NDSVTSKFDNLGCRSLIDGIKRATDVMTAGVAVVAGYGVGKGCACALRGFGARVI 240
QY 241 ITEIDPINALQAAMEGYEVTTMDEACQEGNIFVTTTGCIDIIILGRHFEQMKDDAIVCNIG 300
DB 241 ITEIDPINALQAAMEGYEVTTMDEACQEGNIFVTTTGCIDIIILGRHFEQMKDDAIVCNIG 300
QY 301 HFDVEIDVKWLNENAVEKVNIPQVDYRLKNGRRRIILAEGRVLNLCGAMGHPSPFVMSN 360
DB 301 HFDVEIDVKWLNENAVEKVNIPQVDYRLKNGRRRIILAEGRVLNLCGAMGHPSPFVMSN 360
QY 361 SFTNQVMAQIELTHDPKYPVGVHFLPKLDEAVABHLGKLVNKLTKLTEKQAOYLGM 420
DB 361 SFTNQVMAQIELTHDPKYPVGVHFLPKLDEAVABHLGKLVNKLTKLTEKQAOYLGM 420
QY 421 CDGPFKPDHYRY 432
DB 421 CDGPFKPDHYRY 432

RESULT 3

US-08-896-005-5
; Sequence 5, Application US/08896005
; Patent No. 5854023
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,005
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0337 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 904132
US-08-896-005-5

Query Match 96.6%; Score 2193; DB 2; Length 432;
Best Local Similarity 96.5%; Pred. No. 7.1e-238;
Matches 417; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MSDKLPYKVDIGLAAGWKALDIAENEMPGMLMRERYASGSKPLKGARIAGCLHMTVET 60

Db 1 MSCLKPYKADIGLAAGRKALDIAENEMPGLMRREMTSASKPLKAGIAGCLHMTVET 60
Qy 61 AVLIETLVTLGAENVQSSCNIFSTONHAAATAKAGIPVYANKGETDEEYLWCIEOTLYF 120
Db 61 AVLIETLVALGAENVQSSCNIFSTODHAAATAKAGIPVYANKGETDEEYLWCIEOTLHF 120
Qy 121 KDGPLNMLDDGGDLTNLHTKYPLLPGIRGISEBTITGVNLYKQWANGILKVPAINV 180
Db 121 KDGPLNMLDDGGDLTNLHTKYPLLPGIRGISEBTITGVNLYKQWANGILKVPAINV 180
Qy 181 NDSVTKSFDNLYGCRSLIDGKRATVMIAGKAVVAGYGVGKCAQALRGFGARVI 240
Db 181 NDSVTKSFDNLYGCRSLIDGKRATVMIAGKAVVAGYGVGKCAQALRGFGARVI 240
Qy 241 ITEIDPINALQAMGEYVTTMDEACQEGNI FVTTTGCIDIILGRHFEQMKODAIVCNIG 300
Db 241 ITEIDPINALQAMGEYVTTMDEACQEGNI FVTTTGCVDIILGRHFEQMKODAIVCNIG 300
Qy 301 HFDVEIDVKWLNENAVEKVNIPQVDYRLKNGRRILLAEGRVLNLCAMGHPSPFWSN 360
Db 301 HFDVEIDVKWLNENAVEKVNIPQVDYRLKNGRRILLAEGRVLNLCAMGHPSPFWSN 360
Qy 361 SFTNQVMAQIELMTHDPKYPVGVHFLPKKLDEAVAEHLGKLVNKLTKLTKTEKQAQYLGMS 420
Db 361 SFTNQVMAQIELMTHDPKYPVGVHFLPKKLDEAVAEHLGKLVNKLTKLTKTEKQAQYLGMP 420
Qy 421 CDGPKPKPDHYRY 432
Db 421 INGPKPKPDHYRY 432

RESULT 4
US-08-930-894-2
; Sequence 2, Application US/08930894
; Patent No. 6037524
; GENERAL INFORMATION:
; APPLICANT: GREENLAND, Andrew James
; APPLICANT: DRAPER, John
; APPLICANT: SKIPSEY, Marc
; APPLICANT: WARNER, Simon
; TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEIN HYDROLASE PROMOTER
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutor
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,894
; FILING DATE: 09-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00882
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9507381.3
; FILING DATE: 10-APR-1995
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-930-894-2

Query Match 56.8%; Score 1289; DB 3; Length 485;
Best Local Similarity 56.1%; Pred. No. 5.1e-136;
Matches 265; Conservative 55; Mismatches 106; Indels 46; Gaps 5;
Qy 7 YKVADIGLAAGRKALDIAENEMPGLMRREMTSASKPLKAGIAGCLHMTVETAVLIET 66
Db 14 YKVKDMSQADFGLRIELAEVEMPGMACRAEFGPAQPFKAKITGSLHMTTQTAVLIET 73
Qy 67 LVTLGAENVQSSCNIFSTONHAAATAKAGIPVYANKGETDEEYLWCIEOTLYF 125
Db 74 LVALGAEVQSSCNIFSTODHAAATAKAGIPVYANKGETDEEYLWCIEOTLYF 133
Qy 126 NMILDGGDLTNLH-----TKYP 144
Db 134 DLIVDDGGDTLLIHEGVKAESEYKTKMPDPASTDNAEFOI VLTIIIRDLGLKVPDPTKYR 193
Qy 145 QLLPGIRGISEBTITGVNLYKQWANGILKVPAINVDSVTKSKEDNLYGCRSLIDGK 204
Db 194 KMKDRIVGVSEETITGVNLYKQWANGILKVPAINVDSVTKSKEDNLYGCRSLIDGK 253
Qy 205 RATDVMIAAGKAVVAGYGVGKCAQALRGFGARVIITEIDPINALQAMGEYVTTMDE 264
Db 254 RATDVMIAAGKAVVAGYGVGKCAQALRGFGARVIITEIDPINALQAMGEYVTTMDE 313
Qy 265 AQEGNIFVTTTGCIDIILGRHFEQMKODAIVCNIGHFDEIDVKWLNENAVEKVNIPK 323
Db 314 VVSEADIFVTTTGNKDIIMLDHMRKMNNAIVCNIGHFDEIDVKWLNENAVEKVNIPK 373
Qy 324 QVDYRL-KNGRRILLAEGRVLNLCAMGHPSPFWSNFTNQVMAQIELMTH--PDKYP 380
Db 374 QTDWRVPETNGTIIVLAEGRLNLCATGHPSPFWSNFTNQVMAQIELMTH--PDKYP 433
Qy 381 VGVHFLPKKLDEAVAEHLGKLVNKLTKLTKTEKQAQYLGMSCDGPKPKPDHYRY 432
Db 434 KKVTVLPKHLDEKVAALHLGKLVNKLTKLTKLTKTEKQAQYLGMSCDGPKPKPDHYRY 485

RESULT 5
US-09-252-991A-23501
; Sequence 23501, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23501
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23501

Query Match 55.0%; Score 1249.5; DB 4; Length 502;
Best Local Similarity 56.5%; Pred. No. 1.5e-131;
Matches 261; Conservative 59; Mismatches 101; Indels 41; Gaps 9;
Qy 7 YKVADIGLAAGRKALDIAENEMPGLMRREMTSASKPLKAGIAGCLHMTVETAVLIET 66
Db 46 YKVADITLAAAGRRRLIIAEESEMPGLURRYAGQQPLKGAIKLIGSLHMTTQTAVLIET 105
Qy 67 LVTLGAENVQSSCNIFSTONHAAATAKAGIPVYANKGETDEEYLWCIEOTLYF 123
Db 106 LVALGAEVQSSCNIFSTODHAAATAKAGIPVYANKGETDEEYLWCIEOTLYF 164
Qy 124 PLNMILDGGDLTNLHTKYPLLPGIRGISEBTITGVNLYKQWANGILKVPAINVDS 183

Db 165 DANVLDDGGDLTEILHKKYQOMLERIHGITEETTTGVHRLDMLKNGALKVPAINVND 224
Qy 184 VTKSKENLYGCRSLIDGKRTDVMIAKVAAGVGVGKCAQALRGFGARVITTE 243
Db 225 VTKSKDNKYGCRHSLNDAIKRTDHLGSKQALVIGYGVGKGSQSLRQEGMIVKVAE 284
Qy 244 IDPINALQAAMEGYEVTT-MDEACQEG-----NIFVTTTGCIDILGRHFEQ 289
Db 285 VDFICAMQACMDGFEVSPYKNGINDGTEASIDAALLGKIDILVTTGNVNC DANMLKA 344
Qy 290 MKDDAIVCNIGHDFEIDVKMLNEN-AVEKNVKKPV-----DRLKNGRRRIILLA 340
Db 345 LKRAVVCNIGHDFEIDAFKRWAWAEV--KPQVHKIHRGTGKDFDAHNDYLLILA 402
Qy 341 EGRVLNLCAMGHPSFVMSNSFTNOVMAQIELWTHDPKYP-----VGWHFLPKKL 390
Db 403 EGRVLNLCAMGHPSFVMSNSFTNOVMAQIELWTHDPKYP-----VGWHFLPKKL 390
Qy 391 DEAVAHAHLKLVKLTETKAOAYLGMSCDGPFKPDHRY 432
Db 461 DEEVALEVMKFGGVVTLTPKQAEVIGSVGEGPFKPDYRY 502

RESULT 6.

US-09-328-352-4600
; Sequence 4600, Application US/09328352
; Patent No. 6562958

; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4600

; LENGTH: 463
; TYPE: PRT

; ORGANISM: Acinetobacter baumannii
US-09-328-352-4600

Query Match 53.8%; Score 1222; DB 4; Length 463;
Best Local Similarity 56.2%; Pred. No. 1.6e-128;
Matches 255; Conservative 62; Mismatches 105; Indels 32; Gaps 8;

Qy 7 YKVADIGLAAGKALDIAENEMPGLMRMRYSASKPLKGARIAGCLHMTVETAVLIET 66
Db 14 YKVADISLADYGRKEIKLAEAPALIGLRKYAASKPLAGAKILGCIHMTIQTAVLIET 73
Qy 67 LVTGAEVOWSSCNIFSTONHAAAAIAKAGIPVYAWKGETDEEYLWCIEOTLYFKDGP-- 124
Db 74 LVELGAEVWTSNIFSTONHAAAAIAAGIPVFAWKGETEEYVWCLSEQQNVNGQPD 133
Qy 125 LNMILDDGDLNLHITKYPQLLPGIRGISEETTTGVHNLKYMANGILKVPAINVND 184
Db 134 ANMILDDGDLNLHITKYPQLLPGIRGISEETTTGVHNLKYMANGILKVPAINVND 193
Qy 185 TSKKFNLYGCRSLIDGKRTDVMIAKVAAGVGVGKCAQALRGFGARVITTE 244
Db 194 TSKKDNKYGCRHSLNDAIKRTDMLSGRRALVIGYGVGKGSQSLRQEGMIVRVTEV 253
Qy 245 DPINALQAAMEGYEVTT-MDEACQEG-----NIFVTTTGCIDILGRHFEQ 290
Db 254 DFCAMQACMDGFEVSPYKNGINDGTEASIDAALLGKIDILVTTGNVNC DANMLDS 313
Qy 291 KDDAIVCNIGHDFEIDVKMLNENAVEKNVKKPV-----DRLKNGRRRIILLA 348
Db 314 KAGAVVCNIGHDFEIDAFKRWAWAEV--KPQVHKIHRGTGKDFDAHNDYLLILA 371
Qy 349 CAMGHPSFVMSNSFTNOVMAQIELWTHDPKYP-----VGWHFLPKKLDEAVAHAH 398
Db 372 NATGHPSRVMSNSFTNOVMAQIELWTHDPKYP-----VGWHFLPKKLDEAVAHAH 429

Qy 399 LGLKLVKLTETKAOAYLGMSCDGPFKPDHRY 432
Db 430 VAGFGVLTQLTQEQADYLGIAVEGPFKSDAYK 463

RESULT 7

US-08-896-005-3
; Sequence 3, Application US/08896005
; Patent No. 5854023

; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Preeti

; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE

; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive

; CITY: Palo Alto
; STATE: CA

; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/896,005
; FILING DATE: Filed Herewith

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0337 US
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 504 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear

; IMMEDIATE SOURCE:
; LIBRARY: GenBank

; CLONE: 969078
US-08-896-005-3

Query Match 50.6%; Score 1149.5; DB 2; Length 504;
Best Local Similarity 51.5%; Pred. No. 2.8e-120;
Matches 218; Conservative 83; Mismatches 121; Indels 1; Gaps 1;

Qy 9 VADIGLAAGKALDIAENEMPGLMRMRYSASKPLKGARIAGCLHMTVETAVLIETLV 68
Db 70 VKSISKSAFGRREIEIAESEMFGIMTLRKARDEKPLKGANIVGCTHVNQAQSAVLIETLV 129
Qy 69 TLGAEVOWSSCNIFSTONHAAAAIAKAGIPVYAWKGETDEEYLWCIEOTLYFKDGPLNMI 128
Db 130 QLGAIVRAACNIVSTQNAVAALAEAGIPFAWGETEEBFWCLDRAIYSDGHPNLI 189
Qy 129 LDDGGDLNLHITKYPQLLPGIRGISEETTTGVHNLKYMANGILKVPAINVND 188
Db 190 LDDGGDLNLHITKYPQLLPGIRGISEETTTGVHNLKYMANGILKVPAINVND 249
Qy 189 FNLGCRSLIDGKRTDVMIAKVAAGVGVGKCAQALRGFGARVITTEIDPTN 248
Db 250 FDTFTCRDLSILDSUKRTTDMFGGKQVVICGIVGVGKGAQSLKGGQGCIVVTEVDPTC 309
Qy 249 ALQAAMEGYEVTTMDEACQEGNIFVTTTGCIDILGRHFEQMKDDAIVCNIGHDFEIDV 308

Db 310 ALQAAADGFRVRLNEVIRTDVVVATGKNVITRDHNRMKNGCILCNMGHSCSEIDV 369
Qy 309 KWLNEAENAVKNIKPOVDRLKNGRRIILLAEGRVLNLCGAMGHPSPFVMSNSFTNQVMA 368
Db 370 NGLHTPELTWVRVRSQVDHIRMWDGRMIILLAEGRVLNLSGST-ISSFVSVASSTQALA 428
Qy 369 QIELWTHDPKYPVGVHFLPKKLDDEAVAEAHGLKLNKVLTKLTBKQAQYLGMSCDGPPKPD 428
Db 429 LIELSAPGRYKSDVYLLPKQNDYVYASLHLATFDHAHLTDLTDEQSKPGLNKGAGPFKAN 488
Qy 429 HVR 431
Db 489 YVR 491

RESULT 8
US-08-896-005-1
; Sequence 1, Application US/08896005
; Patent No. 5854023
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,005
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0337 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADTUT04
CLONE: 1519044
US-08-896-005-1

Query Match 50.5%; Score 1146; DB 2; Length 500;
Best Local Similarity 51.3%; Pred. No. 6,7e-120;
Matches 218; Conservative 84; Mismatches 121; Indels 2; Gaps 2;
Qy 9 VADIGLAWGRKALDIAENEMPGLMRRYRSASKPLKGARIAGCLHMTVETAVLIETLV 68
Db 77 VKNIQAERFRRIETAEQMSALISLRKAQEKPLAGAKIVGCTHTTAQAVLIETLC 136
Qy 69 TLGAEVQWSSCNFSTONHAAAAIAKAGIPVYAWKGETDEYLCWIEQTLVFKDGLNMI 128

Db 137 ALGAQCRWSACNIYSTQNEVAALAEAGVAVPAWKGESEDDFWMCIDRCVNMHGWQANMI 196
Qy 129 LDGGDLTNLIHTKYTPOLLPGIRIGISETTTGVHNLKXMGANGILKVPAINVNDVYTKSK 188
Db 197 LDGGDLTHWCKTIPNVFKIRGIVERSTGVHRLYQLSKAGKLCVPAWNVNDVYTKOK 256
Qy 189 FDNLYCCRESLDIGIKRATDVMIAGKAVVAGYGVGVGKCAQALRGFGARVITEIDPIN 248
Db 257 FDNLYCCRESLDGLKRTTDMVFGGQVWVCGYGVGKCAALGALGAIVVITEIDPIC 316
Qy 249 ALQAAAMEGYVTTMBEACQEGNIFVTTTCIDIIILGRHPEQMKDDAIVCNIGHFQVEIDV 308
Db 317 ALQACMDGFRVVKLNEVIRQVDVITCTGNKVNVTREHLDRMKNSCIVCNMGHNSIDEV 376
Qy 309 KWLNEAENAVKNIKPOVDRLKNGRRIILLAEGRVLNLCGAMGHPSPFVMSNSFTNQVMA 368
Db 377 TSLRTPELTWVRVRSQVDHIRMWDGRMIILLAEGRVLNLSGST-VPTFVLSITATTQALA 435
Qy 369 QIELWTHPD-KYPVGVHFLPKKLDDEAVAEAHGLKLNKVLTKLTBKQAQYLGMSCDGPPKPD 427
Db 436 LIELYNAPEGRYKQDVYLLPKQNDYVYASLHLPSFPAHLTDLTDDQAKYLGKNGGPPKP 495
Qy 428 DHYR 432
Db 496 NYR 500

RESULT 9
US-08-204-740-7
; Sequence 7, Application US/08204740
; Patent No. 5753432
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrei
; APPLICANT: Kazarov, Alexander
; APPLICANT: Mazon, Ilya
; TITLE OF INVENTION: Methods for Identifying Genetic
; TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
; TITLE OF INVENTION: Growth in Cancer Cells
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allgretti & Witcoff, Ltd.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,740
FILING DATE: 04-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5753432nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-204-740-7
Query Match 18.5%; Score 421; DB 1; Length 97;

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Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDKLPYKVDIGLAAGWKALDIAENEMPGMLMRERYASAKPLKGARIAGCLHMTVET 60
Db 16 MSDKLPYKVDIGLAAGWKALDIAENEMPGMLMRERYASAKPLKGARIAGCLHMTVET 75
QY 61 AVLIETLVTLGAEVQWSSCNIF 82
Db 76 AVLIETLVTLGAEVQWSSCNIF 97

RESULT 10
US-09-081-167A-7
; Sequence 7, Application US/09081167A
; Patent No. 6083745
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrei
; APPLICANT: Kazarov, Alexander
; APPLICANT: Mazo, Ilya
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Methods for Identifying Genetic
; TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
; TITLE OF INVENTION: Growth in Cancer Cells
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,167A
; FILING DATE: 18-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6083745nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-KK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-081-167A-7

Query Match 18.5%; Score 421; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDKLPYKVDIGLAAGWKALDIAENEMPGMLMRERYASAKPLKGARIAGCLHMTVET 60
Db 16 MSDKLPYKVDIGLAAGWKALDIAENEMPGMLMRERYASAKPLKGARIAGCLHMTVET 75
QY 61 AVLIETLVTLGAEVQWSSCNIF 82
Db 76 AVLIETLVTLGAEVQWSSCNIF 97

RESULT 11
US-09-081-395-7
; Sequence 7, Application US/09081395
; Patent No. 6083746
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrei
; APPLICANT: Kazarov, Alexander
; APPLICANT: Mazo, Ilya
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Methods for Identifying Genetic
; TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
; TITLE OF INVENTION: Growth in Cancer Cells
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,395
; FILING DATE: 18-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6083746nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-KK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-081-395-7

Query Match 18.5%; Score 421; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDKLPYKVDIGLAAGWKALDIAENEMPGMLMRERYASAKPLKGARIAGCLHMTVET 60
Db 16 MSDKLPYKVDIGLAAGWKALDIAENEMPGMLMRERYASAKPLKGARIAGCLHMTVET 75
QY 61 AVLIETLVTLGAEVQWSSCNIF 82
Db 76 AVLIETLVTLGAEVQWSSCNIF 97

RESULT 12
US-09-416-833-7
; Sequence 7, Application US/09416833
; Patent No. 6197521
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrei
; APPLICANT: Kazarov, Alexander
; APPLICANT: Mazo, Ilya
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Methods for Identifying Genetic
; TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
; TITLE OF INVENTION: Growth in Cancer Cells
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allgretti & Witcoff, Ltd.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
```

[illegible]

```

; APPLICANT: Mazo, Ilya
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Methods for Identifying Genetic
; TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
; TITLE OF INVENTION: Growth in Cancer Cells
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,167A
; FILING DATE: 18-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6083745nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-KK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-081-167A-9

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Query Match      17.1%; Score 388; DB 3; Length 95;
Best Local Similarity 92.7%; Pred. No. 8.7e-36;
Matches 76; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy      1 MSDKLPYKVADIGLAANGRKALDIAENEMPGLMREMYASAKPLKGARIAGCLHMTVET 60
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      14 MSDKLPYKVADIGLAANGRKALDIAENEMPGLMREMYASAKPLKGARIAGCLHMTVET 73

Qy      61 AVLIETLVTLGAEVQWSSCNIF 82
        |||||  |||||  |||||  |||||
Db      74 AVLIETKVALGAEARWSSCNIF 95

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Search completed: December 30, 2003, 10:43:06
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:38:13 ; Search time 41 Seconds
(without alignments)
2718.993 Million cell updates/sec

Title: US-10-043-787-1

Perfect score: 2271

Sequence: 1 MSKLPYKVADIGLAAGRK.....QAQYLGMSCDGPFKPDHYRY 432

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2190	96.4	432	Q8HXL1	Q8hxl1 sus scrofa
2	1819.5	80.1	432	Q9VXV5	Q9vxv5 drosophila
3	1805.5	79.5	432	Q8MZ11	Q8mz11 drosophila
4	1665	73.3	324	Q8BP17	Q8bp17 mus musculus
5	1522.5	67.0	436	Q8XV1	Q8xv1 leptospira
6	1516	66.8	471	Q8KEG8	Q8keg8 chlorobium
7	1476	65.0	285	Q9HAU6	Q9haue6 homo sapien
8	1401	61.7	480	Q8PC85	Q8pc85 xanthomonas
9	1393	61.3	469	Q8GGL7	Q8gg17 streptomyce
10	1386	61.0	480	Q8PP84	Q8pp84 xanthomonas
11	1309.5	57.7	463	Q8KV9	Q8kv9 uncultured
12	1305	57.5	466	Q8FXZ7	Q8fxz7 brucella su
13	1291	56.8	485	Q8LE20	Q8le20 arabidopsis
14	1277	56.2	485	Q94929	Q94929 arabidopsis
15	1274	56.1	485	Q8LPS8	Q8lps8 arabidopsis
16	1274	56.1	485	Q944K5	Q944k5 arabidopsis

17	1274	56.1	485	10	Q9LK36	Q9lk36 arabidopsis
18	1246	54.9	450	10	Q42939	Q42939 nicotiana s
19	1238	54.5	474	16	Q8NSC4	Q8nec4 corynebacte
20	1233	54.3	478	16	Q8FRJ4	Q8frj4 corynebacte
21	1218	53.6	479	5	Q8MUG1	Q8mug1 plasmodium
22	1156.5	50.9	492	5	Q8MYX7	Q8myx7 drosophila
23	1151	50.7	530	4	Q9GPK4	Q9gpk4 homo sapien
24	1151	50.7	597	4	Q9UG84	Q9ug84 homo sapien
25	1149.5	50.6	521	5	Q9VZX9	Q9vzx9 drosophila
26	1147	50.5	508	11	Q8BIH1	Q8bih1 mus musculu
27	916.5	40.4	431	10	Q947H3	Q947h3 petunia hyb
28	797.5	35.1	425	2	Q8GDW5	Q8gdw5 heliobacill
29	797	35.1	429	16	Q8DGC8	Q8dgc8 synechococc
30	789	34.7	312	10	Q9SDP1	Q9sdp1 allium cepa
31	786	34.6	411	17	Q8PUO4	Q8puq4 methanosaar
32	779	34.3	411	17	Q8TRAS	Q8tra5 methanosaar
33	752	33.1	143	4	Q8ZL13	Q8z13 homo sapien
34	581	25.6	195	10	Q9XSL8	Q9xe18 alexandrium
35	527	23.2	181	2	Q9R6R6	Q9r6r6 mycobacteri
36	511	22.5	218	4	Q43210	Q43210 homo sapien
37	450	19.8	202	4	Q9BTL0	Q9bt10 homo sapien
38	449	19.8	232	10	Q8W530	Q8w530 zea mays (m
39	423	18.6	171	10	Q8SP98	Q8sp98 solanum cha
40	423	18.6	500	16	Q8GSA1	Q8gsa1 bifidobacte
41	409.5	18.0	140	2	Q9R6R7	Q9r6r7 mycobacteri
42	377	16.6	121	10	Q41974	Q41974 arabidopsis
43	362	15.9	90	10	Q9M4V0	Q9m4v0 lupinus lut
44	336	14.8	102	10	Q9XF45	Q9xf45 gossypium h
45	324	14.3	96	2	Q93CC0	Q93cc0 mycobacteri

ALIGNMENTS

RESULT 1

Q8HXL1	PRELIMINARY;	PRT;	432 AA.
ID	Q8HXL1		
AC	Q8HXL1;		
DT	01-MAR-2003 (Tremblrel. 23, Created)		
DT	01-MAR-2003 (Tremblrel. 23, Last sequence update)		
DT	01-MAR-2003 (Tremblrel. 23, Last annotation update)		
DE	S-adenosylhomocysteine hydrolase (EC 3.3.1.1).		
GN	AHCY.		
OS	Sus scrofa (Pig).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
OX	NCBI_TaxID=9823;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22326073; PubMed=12438749;		
RA	Leeb T.; Rohrer G.A.;		
RT	"Characterization and chromosomal assignment of the porcine AHCY gene		
RT	for S-adenosylhomocysteine hydrolase.";		
RL	Cytogenet. Genome Res. 97:116-119(2002).		
DR	EMBL; AJ422131; CAD19504.1; -.		
KW	Hydrolase.		
SQ	SEQUENCE 432 AA; 47694 MW; 0B756B5F83F6B90E CRC64;		

Query Match 96.4%; Score 2190; DB 6; Length 432;
Best Local Similarity 96.3%; Pred. NO. 1.4e-159;
Matches 416; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY	1	MSKLPYKVADIGLAAGRKALDIENEMPGMLMRERYSASKPLKAGIAGCLHMTVET	60
DB	1	MSKLPYKVADIGLAAGRKALDIENEMPGMLMRERYSASKPLKAGIAGCLHMTVET	60
QY	61	AVLIETLVLTGAEVOWSSCNIFSTQNHAAAAIAKAGIPYAWKGETDEBYLWCIEQTLYP	120
DB	61	AVLIETLVLTGAEVOWSSCNIFSTQNHAAAAIAKAGIPYAWKGETDEBYLWCIEQTLYP	120
QY	121	KDGPLNMLDDGGDLTNLHTKYPQLLPQIRIGISEBTGGVHNLKPMANGILKVPAINV	180
DB	121	KDGPLNMLDDGGDLTNLHTKYPQLLPQIRIGISEBTGGVHNLKPMANGILKVPAINV	180

QY 181 NDSVTSKPNLYGCRSLIDGKIRATDVMIAGKAVVAGYGVGKCAQALGFGARVI 240
 DB 181 NDSVTSKPNLYGCRSLIDGKIRATDVMIAGKAVVAGYGVGKCAQALGFGARVI 240
 QY 241 ITEIDPINALQAAMEGYEVTMDACQEGNIFVTTTCGIDIIILGRHFEQMKDDAIVCNIG 300
 DB 241 ITEIDPINALQAAMEGYEVTMDACQEGNIFVTTTCGIDIIILGRHFEQMKDDAIVCNIG 300
 QY 301 HFDVEIDVKWLNENAVEKVNIPQVDYRLKNGRRILLAEGLVNLGCAMGHPSPVMSN 360
 DB 301 HFDVEIDVKWLNENAVEKVNIPQVDYRLKNGRRILLAEGLVNLGCAMGHPSPVMSN 360
 QY 361 SFTNQVMAQIELWTHDPKYPVGVHFLPKLDEVAEHLGKLVNKLTKTEKQAQYLGM 420
 DB 361 SFTNQVMAQIELWTHDPKYPVGVHFLPKLDEVAEHLGKLVNKLTKTEKQAQYLGM 420
 QY 421 CDGPFKPDHYRY 432
 DB 421 REGPFKPDHYRY 432
 RESULT 2
 Q9VXV5 PRELIMINARY; PRT; 432 AA.
 AC Q9VXV5
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Ahcyl13 protein (EC 3.3.1.1) (Adenosylhomocysteinase) (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase).
 GN AHXY13 OR CG11654.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.B.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Borzhan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: ADENOSYLHOMOCYSTEINE IS A COMPETITIVE INHIBITOR OF S-
 ADENOSYL-L-METHIONINE-DEPENDENT METHYL TRANSFERASE REACTIONS;
 THEREFORE ADENOSYLHOMOCYSTEINE MAY PLAY A KEY ROLE IN THE
 CONTROL OF METHYLATIONS VIA REGULATION OF THE INTRACELLULAR
 CONCENTRATION OF ADENOSYLHOMOCYSTEINE (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: S-ADENOSYL-L-HOMOCYSTEINE + H(2)O = ADENOSINE
 + L-HOMOCYSTEINE.
 CC -!- COFACTOR: NAD (BY SIMILARITY).
 CC -!- PATHWAY: ACTIVATED METHYL CYCLE.
 CC -!- SIMILARITY: BELONGS TO THE ADENOSYLHOMOCYSTEINASE FAMILY.
 DR EMBL; AF003499; AAF48453.1; -.
 DR HSSP; P10760; 1B3R.
 DR FlyBase; FBgn0014455; Ahcyl13.
 DR InterPro; IPR000043; Ado_hcyase.
 DR Pfam; PF00670; AdoHcyase; 1.
 DR TIGRFAMs; TIGR00936; ahcy; 1.
 DR PROSITE; PS00738; ADOHCYASE_1; 1.
 DR PROSITE; PS00739; ADOHCYASE_2; 1.
 KW Hydrolase; NAD; One-carbon metabolism.
 SQ SEQUENCE 432 AA; 47366 MW; 2977DAF12B40C324 CRC64;
 Query Match 80.1%; Score 1819.5; DB 5; Length 432;
 Best Local Similarity 80.7%; Pred. No. 3.5e-131;
 Matches 347; Conservative 28; Mismatches 54; Indels 1; Gaps 1;
 QY 4 KLPYKVADIGLAAMGRKALDIAENEMPGIMRREYSASKPLKGARIACGLHMTVETAVL 63
 DB 3 KESYKVADISLAEGWGRKAIITAEENEMPGIMRREYSASKPLKGARIITGCLHMTVQTAVL 62
 QY 64 IETLVTLGAEVQWSSCNIFSTONHAAATAKAGIPVYAWKGTDEEYLWCIEQTLYFKDG 123
 DB 63 IETLVELGNOVQWSSCNIFSTODNAAATAATGVVYAWKGTDEEYMWCIETLVFPDG 122
 QY 124 -PLNMILDDGGDLTNLHNTKYPQLLPGRIGISETTTGVHNLVYQWANGILKVPAINVD 182
 DB 123 QPLNMILDDGGDLTNLHNTKYPQLLPGRIGISETTTGVHNLVYQWANGILKVPAINVD 182
 QY 183 SVTSKFNLYGCRSLIDGKIRATDVMIAGKAVVAGYGVGKCAQALGFGARVIIT 242
 DB 183 SVTSKFNLYGCRSLIDGKIRATDVMIAGKAVVAGYGVGKCAQALGFGARVIIT 242
 QY 243 EIDPINALQAAMEGYEVTMDACQEGNIFVTTTCGIDIIILGRHFEQMKDDAIVCNIGHF 302
 DB 243 EVDPINALQAAMEGYEVTMDACQEGNIFVTTTCGIDIIILGRHFEQMKDDAIVCNIGHF 302
 QY 303 DVEIDVKWLNENAVEKVNIPQVDYRLKNGRRILLAEGLVNLGCAMGHPSPVMSNSF 362
 DB 303 DIEIDVDWLNENAVEKVNIPQVDYRLKNGRRILLAEGLVNLGCAMGHPSPVMSNSF 362
 QY 363 TNQVMAQIELWTHDPKYPVGVHFLPKLDEVAEHLGKLVNKLTKTEKQAQYLGMSCD 422
 DB 363 TNQVLAQIELWTHDPKYPVGVHFLPKLDEVAEHLGKLVNKLTKTEKQAQYLGMSCD 422
 QY 423 GPFKPDHYRY 432
 DB 423 GPFKPDHYRY 432
 RESULT 3
 Q9WZ11 PRELIMINARY; PRT; 432 AA.
 ID Q9WZ11
 AC Q9WZ11
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE GM02466p.
 GN AHXY13 OR CG11654.

SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Body;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
DR EMBL; AK075629; BAC35867.1; --
FT NON TER 1
SQ SEQUENCE 324 AA; 36040 MW; 370014DE8B2BEFDB CRC64;

Query Match 73.3%; Score 1665; DB 11; Length 324;
Best Local Similarity 97.2%; Pred. No. 1.6e-119;
Matches 315; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 109 EYLWCIEOTLHFKDGLPLNMLDDGGDLTNLHTKYPOLLPGIRGISSETTTGVHNLKYM 168
DB 1 EYLWCIEOTLHFKDGLPLNMLDDGGDLTNLHTKYPOLLPGIRGISSETTTGVHNLKYM 60
QY 169 ANGILKVPAINVNDVSTKSKFDNLYGCRSLIDGKIBATDVMIAKGVAVAGYDVGKGC 228
DB 61 SNGILKVPAINVNDVSTKSKFDNLYGCRSLIDGKIBATDVMIAKGVAVAGYDVGKGC 120
QY 229 AQAALGFGARVITITDIPINALQAAMEGYEVTTWDEACQEGNIPVTTTCIDILGRHPE 288
DB 121 AQAALGFGARVITITDIPINALQAAMEGYEVTTWDEACQEGNIPVTTTCIDILGRHPE 180
QY 289 OMKDDAIVCNIGHPDVEIDVKWLNENAVEKYNIPQVDVRYLKNKGRRIILLAEGRVLNLG 348
DB 181 OMKDDAIVCNIGHPDVEIDVKWLNENAVEKYNIPQVDVRYLKNKGRRIILLAEGRVLNLG 240
QY 349 CAMGHPSPFMSNSFTNQVMAQIELWTHDPKYPVGVHFLPKLDEAVAHLGKLNVLTK 408
DB 241 CAMGHPSPFMSNSFTNQVMAQIELWTHDPKYPVGVHFLPKLDEAVAHLGKLNVLTK 300
QY 409 LTKAQYVLGMSGCDGPFKPDHYRY 432
DB 301 LTKAQYVLGMPINGPFKPDHYRY 324

RESULT 5
Q8EXV1 PRELIMINARY; PRT; 436 AA.
AC Q8EXV1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE S-adenosylhomocysteine hydrolase.
GN LB106.
OS Leptosira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE011599; AA051665.1; --
KW Hydrolase; Complete proteome.
SQ SEQUENCE 436 AA; 48233 MW; 1E73AE26ECBDFAC1 CRC64;

Query Match 67.0%; Score 1522.5; DB 16; Length 436;
Best Local Similarity 69.2%; Pred. No. 2.1e-108;
Matches 297; Conservative 48; Mismatches 81; Indels 3; Gaps 2;

QY 5 LPYKVADICLAAGWGRKALDIENENPGLMRMRYSKPLKGARIAGCLHMTVETAVLI 64
DB 10 LSYKVKDLSQAEWGQEIILAEKEMPGLMALRQYKGGKPLAGARIAGSLHMTIQTAVLI 69
QY 65 ETLVTLGAEVQWSSCNIFSTQNHAAAAIAKAGIPYAWKGTDEBYLWCIEQTLFYKDPG 124
DB 70 ETLVTLGAEVQWSSCNIFSTQNHAAAAIAKAGIPYAWKGTDEBYLWCIEQTLFYKDPG 129
DB NCBI_TaxID=10090;
RN [1]

SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Body;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
DR EMBL; AK075629; BAC35867.1; --
FT NON TER 1
SQ SEQUENCE 324 AA; 36040 MW; 370014DE8B2BEFDB CRC64;

Query Match 73.3%; Score 1665; DB 11; Length 324;
Best Local Similarity 97.2%; Pred. No. 1.6e-119;
Matches 315; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 109 EYLWCIEOTLHFKDGLPLNMLDDGGDLTNLHTKYPOLLPGIRGISSETTTGVHNLKYM 168
DB 1 EYLWCIEOTLHFKDGLPLNMLDDGGDLTNLHTKYPOLLPGIRGISSETTTGVHNLKYM 60
QY 169 ANGILKVPAINVNDVSTKSKFDNLYGCRSLIDGKIBATDVMIAKGVAVAGYDVGKGC 228
DB 61 SNGILKVPAINVNDVSTKSKFDNLYGCRSLIDGKIBATDVMIAKGVAVAGYDVGKGC 120
QY 229 AQAALGFGARVITITDIPINALQAAMEGYEVTTWDEACQEGNIPVTTTCIDILGRHPE 288
DB 121 AQAALGFGARVITITDIPINALQAAMEGYEVTTWDEACQEGNIPVTTTCIDILGRHPE 180
QY 289 OMKDDAIVCNIGHPDVEIDVKWLNENAVEKYNIPQVDVRYLKNKGRRIILLAEGRVLNLG 348
DB 181 OMKDDAIVCNIGHPDVEIDVKWLNENAVEKYNIPQVDVRYLKNKGRRIILLAEGRVLNLG 240
QY 349 CAMGHPSPFMSNSFTNQVMAQIELWTHDPKYPVGVHFLPKLDEAVAHLGKLNVLTK 408
DB 241 CAMGHPSPFMSNSFTNQVMAQIELWTHDPKYPVGVHFLPKLDEAVAHLGKLNVLTK 300
QY 409 LTKAQYVLGMSGCDGPFKPDHYRY 432
DB 301 LTKAQYVLGMPINGPFKPDHYRY 324

RESULT 5
Q8EXV1 PRELIMINARY; PRT; 436 AA.
AC Q8EXV1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE S-adenosylhomocysteine hydrolase.
GN LB106.
OS Leptosira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE011599; AA051665.1; --
KW Hydrolase; Complete proteome.
SQ SEQUENCE 436 AA; 48233 MW; 1E73AE26ECBDFAC1 CRC64;

Query Match 67.0%; Score 1522.5; DB 16; Length 436;
Best Local Similarity 69.2%; Pred. No. 2.1e-108;
Matches 297; Conservative 48; Mismatches 81; Indels 3; Gaps 2;

QY 5 LPYKVADICLAAGWGRKALDIENENPGLMRMRYSKPLKGARIAGCLHMTVETAVLI 64
DB 10 LSYKVKDLSQAEWGQEIILAEKEMPGLMALRQYKGGKPLAGARIAGSLHMTIQTAVLI 69
QY 65 ETLVTLGAEVQWSSCNIFSTQNHAAAAIAKAGIPYAWKGTDEBYLWCIEQTLFYKDPG 124
DB 70 ETLVTLGAEVQWSSCNIFSTQNHAAAAIAKAGIPYAWKGTDEBYLWCIEQTLFYKDPG 129
DB NCBI_TaxID=10090;
RN [1]

SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Body;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
DR EMBL; AK075629; BAC35867.1; --
FT NON TER 1
SQ SEQUENCE 324 AA; 36040 MW; 370014DE8B2BEFDB CRC64;

Query Match 73.3%; Score 1665; DB 11; Length 324;
Best Local Similarity 97.2%; Pred. No. 1.6e-119;
Matches 315; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 109 EYLWCIEOTLHFKDGLPLNMLDDGGDLTNLHTKYPOLLPGIRGISSETTTGVHNLKYM 168
DB 1 EYLWCIEOTLHFKDGLPLNMLDDGGDLTNLHTKYPOLLPGIRGISSETTTGVHNLKYM 60
QY 169 ANGILKVPAINVNDVSTKSKFDNLYGCRSLIDGKIBATDVMIAKGVAVAGYDVGKGC 228
DB 61 SNGILKVPAINVNDVSTKSKFDNLYGCRSLIDGKIBATDVMIAKGVAVAGYDVGKGC 120
QY 229 AQAALGFGARVITITDIPINALQAAMEGYEVTTWDEACQEGNIPVTTTCIDILGRHPE 288
DB 121 AQAALGFGARVITITDIPINALQAAMEGYEVTTWDEACQEGNIPVTTTCIDILGRHPE 180
QY 289 OMKDDAIVCNIGHPDVEIDVKWLNENAVEKYNIPQVDVRYLKNKGRRIILLAEGRVLNLG 348
DB 181 OMKDDAIVCNIGHPDVEIDVKWLNENAVEKYNIPQVDVRYLKNKGRRIILLAEGRVLNLG 240
QY 349 CAMGHPSPFMSNSFTNQVMAQIELWTHDPKYPVGVHFLPKLDEAVAHLGKLNVLTK 408
DB 241 CAMGHPSPFMSNSFTNQVMAQIELWTHDPKYPVGVHFLPKLDEAVAHLGKLNVLTK 300
QY 409 LTKAQYVLGMSGCDGPFKPDHYRY 432
DB 301 LTKAQYVLGMPINGPFKPDHYRY 324

RESULT 5
Q8EXV1 PRELIMINARY; PRT; 436 AA.
AC Q8EXV1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE S-adenosylhomocysteine hydrolase.
GN LB106.
OS Leptosira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE011599; AA051665.1; --
KW Hydrolase; Complete proteome.
SQ SEQUENCE 436 AA; 48233 MW; 1E73AE26ECBDFAC1 CRC64;

Query Match 67.0%; Score 1522.5; DB 16; Length 436;
Best Local Similarity 69.2%; Pred. No. 2.1e-108;
Matches 297; Conservative 48; Mismatches 81; Indels 3; Gaps 2;

QY 5 LPYKVADICLAAGWGRKALDIENENPGLMRMRYSKPLKGARIAGCLHMTVETAVLI 64
DB 10 LSYKVKDLSQAEWGQEIILAEKEMPGLMALRQYKGGKPLAGARIAGSLHMTIQTAV

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QY 125 LNMILDDGGDLTNLIHTKYPOLLPGRIGSEETTTGVHNLKYMANGILKVPAINVNDV 184
Db 130 PNMILDDGGDLTAIHEKYPLLSSEIGSEETTTGVKSLYKULKKGELKVPAINVNDV 189
QY 185 TSKFDFNLGCRSLDGIKRAITDVMAGVAVVAGVGVGKCAQALRGFGARVITTEI 244
Db 190 TSKFDFNLGCRSLDGIKRAITDVMAGVAVVAGVGVGKCAQALRGFGARVITTEI 249
QY 245 DPINALQAMGEGYVTTMDACQENIFVTTTCIDIIILGRHPEQKDDAIVCNIGHFDV 304
Db 250 DPICALQAMGEGYVTTMDACQENIFVTTTCIDIIILGRHPEQKDDAIVCNIGHFDV 309
QY 305 EIDVKNL-NENAVKVNIPQVDYRLKNGRRRIILAEGRNLVNLGCMGHPSPVMSNST 363
Db 310 EIQMSRLNNEKGVTKKEIKQVDKYTFDQKSIIVLAEGRLVNLGCMGHPSPVMSNST 369
QY 364 NOVMAQIELWTHDPKYPVGVHFLPKLDEAVAEHLGKLVNKLTKLTKTEKQAOYLGMSCDG 423
Db 370 NOVLAQIELYN--NKVELGVYTLPKHLDKVAALHLEQLGVLRLTKLNQKQADYLVGPING 427
QY 424 PFKPDHYRY 432
Db 428 PFKPDHYRY 436

RESULT 6
Q8KEG8 PRELIMINARY; PRT; 471 AA.
ID Q8KEG8 AC Q8KEG8
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Adenosylhomocysteinease.
GN SAHH OR CT0721.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TLS / ATCC 49652 / DSM 12025;
RX MEDLINE=22103685; PubMed=12093901;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., Deboy R.R., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Unayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).
DR EMBL; AB012843; AAM71958.1; -.
DR TIGR; CT0721; -.
DR InterPro; IPR000043; Ado_hcyase.
DR InterPro; IPR000205; NAD_binding.
DR Pfam; PF00670; AdoHcyase; hcy; 1.
DR TIGRFAMs; TIGR00936; hcy; 1.
DR PROSITE; PS00738; ADHOCYASE_1; 1.
DR PROSITE; PS00739; ADHOCYASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 471 AA; 51949 MW; 31B082405D241047 CRC64;

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Query Match 66.8%; Score 1516; DB 16; Length 471;
Best Local Similarity 64.2%; Pred.No. 7.4e-108;
Matches 300; Conservative 49; Mismatches 76; Indels 42; Gaps 6;

QY 5 LPYKADIGLAAGWKALDIAENEMPGLMRMERYASKPLKGIAGTGLHMTVAVLI 64
Db 8 LDYKADISLAEMGRKEIEIAEKMPGLMATRKYEKKPLAGTAGSLHMTIQTAVLI 67
QY 65 ETLVTLGAEVQWSSCNIFSTQNHAAAIKAGIPVYVANKGETDEEYLWCIEQTLVFKD-- 122

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Db 68 ETLVELGADVRSACNIFSTQDHAAAAIAAAGVPVFAWKGETLDEYVWCTROLLEPEGGL 127
QY 123 GPLNMILDDGGDLTNLIHTKY-----PQLL----- 147
Db 128 GP-NLIVDDGGDLTMIHFGYKIENDPMSMLDKTPGNAEKKALLQQLKAVFAEDNQRWKVV 186
QY 148 -PGIGSIESETTTGVHNLKYMANGILKVPAINVNDVTKSKFDFNLGCRSLDGIKRA 206
Db 187 AAGMGVSEETTTGVHRLYQMMKEGELLFPAINVNDVTKSKFDFNLGCRSLDGIKRA 246
QY 207 TDVMIAGVAVVAGVGVGKCAQALRGFGARVITTEIDPINALQAMGEGYVTTMDAC 266
Db 247 TDVMIAGVAVVAGVGVGKCAQALRGFGARVITTEIDPICALQAMGEGYVTTMEEAV 306
QY 267 QGNIFFVTTTCIDIIILGRHPEQKDDAIVCNIGHFDVDEIDVKWLN--NAVEKVNIPQV 325
Db 307 KEGNIFVTATGNKQVITLDHIKQMRDEATVNCNIGHFDNEIQVDALNNFKGATRIINIKPOV 366
QY 326 DRYRLKNGRRIILAEGRNLVNLGCMGHPSPVMSNSTNOVMAQIELWTHDPKYPVGVHFL 385
Db 367 DKYVFENGNCIYLLAEGRNLVNLGCMGHPSPVMSNSTNQTLLAQIELW--QNDYKVGVTYR 424
QY 385 LPKLDDEAVAEHLGKLVNKLTKLTKTEKQAOYLGMSCDGPFPKPDHYRY 432
Db 425 LPKLDDEAVARLHLGQIGAKLTLLTKEQADYLVGPVGEYKPEHYRY 471

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RESULT 7
Q9H4U6 PRELIMINARY; PRT; 285 AA.
ID Q9H4U6 AC Q9H4U6
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE BK3216D2.1.1 (EC 3.3.1.1) (S-adenosylhomocysteine hydrolase (SAHH),
DE isoform 1) (Adenosylhomocysteinease) (S-adenosyl-L-homocysteine
DE hydrolase) (AdoHcyase).
DE AHCY.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Brown A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ADENOSYLHOMOCYSTEINE IS A COMPETITIVE INHIBITOR OF S-
CC ADENOSYL-L-METHIONINE-DEPENDENT METHYL TRANSFERASE REACTIONS;
CC THEREFORE ADENOSYLHOMOCYSTEINASE MAY PLAY A KEY ROLE IN THE
CC CONTROL OF METHYLATIONS VIA REGULATION OF THE INTRACELLULAR
CC CONCENTRATION OF ADENOSYLHOMOCYSTEINE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: S-ADENOSYL-L-HOMOCYSTEINE + H(2)O = ADENOSINE
CC + L-HOMOCYSTEINE.
CC -!- COFACTOR: NAD (BY SIMILARITY).
CC -!- PATHWAY: ACTIVATED METHYL CYCLE.
CC -!- SIMILARITY: BELONGS TO THE ADENOSYLHOMOCYSTEINASE FAMILY.
DR EMBL; AL356299; CAC09529.1; -.
DR HSSP; P10760; 1B3R.
DR InterPro; IPR000043; Ado_hcyase.
DR Pfam; PF00670; AdoHcyase; 1.
DR PROSITE; PS00738; ADHOCYASE_1; 1.
DR PROSITE; PS00739; ADHOCYASE_2; 1.
KW Hydrolase; NAD; One-carbon metabolism.
SQ SEQUENCE 285 AA; 30871 MW; 762B417FAB54FEB3 CRC64;

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Query Match 65.0%; Score 1476; DB 4; Length 285;
Best Local Similarity 99.6%; Pred.No. 4.2e-105;
Matches 284; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDKLPYKADIGLAAGWKALDIAENEMPGLMRMERYASKPLKGIAGTGLHMTVET 60
Db 1 MSDKLPYKADIGLAAGWKALDIAENEMPGLMRMERYASKPLKGIAGTGLHMTVET 60

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QY 61 AVLIETLVTLGAEVQSSCNIFSTQNHAAAAIAKAGIPVYAWKGETDEEYLWCIEQTLVF 120
DB 61 AVLIETLVTLGAEVQSSCNIFSTQDHAAAAIAKAGIPVYAWKGETDEEYLWCIEQTLVF 120

QY 121 KDGFLNMLDDGGDLNLHITKYQPLLPGIRGISEETTTGVHNLKYMANGILKVPAINV 180
DB 121 KDGFLNMLDDGGDLNLHITKYQPLLPGIRGISEETTTGVHNLKYMANGILKVPAINV 180

QY 181 NDSVTKSKFNLKYGCRSLDGLIKRATDVMIAGKAVVAGYGVGKCAQALRGFGARVI 240
DB 181 NDSVTKSKFNLKYGCRSLDGLIKRATDVMIAGKAVVAGYGVGKCAQALRGFGARVI 240

QY 241 ITEIDPINALQAAMEGYEVTMTDEACQEGNIFVTTCIDIIILGR 285
DB 241 ITEIDPINALQAAMEGYEVTMTDEACQEGNIFVTTCIDIIILGR 285

RESULT 8
Q8PCH5 PRELIMINARY; PRT; 480 AA..
AC Q8PCH5;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DE Adenosylhomocysteinase.
GN SAHH OR KCC0752.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locati E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463(2002).
DR EMBL; AE012174; ANM40067.1; -.
DR InterPro; IPR000043; Ado_hcyase.
DR Pfam; PF00670; AdoHcyase; 1.
DR TIGRPFAMs; TIGR00936; ahcy; 1.
DR PROSITE; PS00738; ADHCYASE_1; 1.
DR PROSITE; PS00739; ADHCYASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 480 AA; 52629 MW; 2F2B6C776D9B9E54 CRC64;

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Query Match 61.7%; Score 1401; DB 16; Length 480;
Best Local Similarity 60.9%; Pred. No. 5e-99;
Matches 285; Conservative 45; Mismatches 96; Indels 42; Gaps 6;

QY 7 YKVADIGLAAGRWKALDIAENMPGLMRMRERYASAKPLKGARIAGCLHMTVETAVLIET 66
DB 13 YKIDISLADWGRKELDIAEHMPGLMSIRKHAQTKPLKDVRLTSLHMTIQTAVLIET 72

QY 67 LVTLGAEVQSSCNIFSTQNHAAAAIAKAGIPVYAWKGETDEEYLWCIEQTLVF--KGGP 124
DB 73 LKDIGANVRVSNIFSTQDHAAAAIAATGTPVFAWKGETLEEYWDCTLDALTFTLPDGT 132

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QY 125 L---NMILDGGDLNLHITKY-----POLL-----PCI----- 150
DB 133 LTGPVLVDDGGDVTLLHKGVELENGSTWDEPASHHEGVIKALLKRVAVVERPGYWAR 192

QY 151 -----RGISEETTTGVHNLKYMANGILKVPAINVNDSTVTKSKFNLKYGCRSLDGLIKR 205
DB 193 VVKDWKGVSEETTTGVHRLYQIAEAGKLLIPAINVNDSTVTKSKFNLKYGCRSLADGLKR 252

QY 206 ATDVMIAGKAVVAGYGVGKCAQALRGFGARVIITEIDPINALQAAMEGYEVTMTDEA 265
DB 253 ANDVMIAGKAVVCGYGVGKGSASLRAYGARVIVTEIDPICALQASMEGFEVNTIEST 312

QY 266 COEGNIFVTTCIDIIILGRHPEOMKDDAIVCNIGHFDVEIDVKWLN--NAVYKVNIKPQ 324
DB 313 LGRGDIYVTTTCNKDIIIVHQLQMKDQAIVCNIGHFDNEIQVDALNALKVGKINIKPQ 372

QY 325 VDRYRLKNGRRRIILAEGRNLVNLGCMGHPSPVMSPTNQVMAQIBLTHTPDKYPGVGH 384
DB 373 VDKYVFGNGNAIFLLADGRLVNLGCATGHPSPVMSNSFANQTLAQIDLWKRDSVEKKVY 432

QY 385 FLPKKLDEAVAHAHLGNVLTLTLEKQAQVYLGMSCDGPPKPDHRY 432
DB 433 ILPKHLDEEVARLHLEKIGVKLTUTLKQDQYLGVDVAGPYRPHRY 480

RESULT 9
Q8GGL7 PRELIMINARY; PRT; 469 AA.
AC Q8GGL7;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Adenosylhomocysteinase.
OS Streptomyces atroolivaceus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=66869;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22336326; PubMed=12446651;
RA Cheng Y.Q., Tang G.L., Shen B.;
RT "Identification and Localization of the Gene Cluster Encoding
RT Biosynthesis of the Antitumor Macrolactam Leinamycin in Streptomyces
RT atroolivaceus S-140";
RL J. Bacteriol. 184:7013-7024(2002).
DR EMBL; AF484556; AAN85548.1; -.
SQ SEQUENCE 469 AA; 51088 MW; 9B1980B1A5FCFA2E CRC64;

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Query Match 61.3%; Score 1393; DB 2; Length 469;
Best Local Similarity 60.8%; Pred. No. 2e-98;
Matches 282; Conservative 58; Mismatches 90; Indels 34; Gaps 6;

QY 2 SDKLPYKVADIGLAAGRWKALDIAENMPGLMRMRERYASAKPLKGARIAGCLHMTVETA 61
DB 7 ADFTDFKVADLSLAAGFGRKEITLAEHMPGLMSIREEYAAAOPLAGARITGSLHMTVQTA 66

QY 62 VLIETLVTLGAEVQSSCNIFSTQNHAAAAIAKAGIPVYAWKGETDEEYLWCIEQTLVF- 120
DB 67 VLIETLVALGADVVRVWVSCNIYSTQDHAAAAIAAANGIPVFAWKGETLEEYWMCTEQALTWP 126

QY 121 -KDGFLNMLDDGGDLNLHITKYQPLLPGIRGISEETTTGVHNLKYMANGILKVPAINV 149
DB 127 GHTGP-NMLDDGGDVTLLHKGVEYRKTGILPEAENELAVVRALLDRSGLDWTAMSSSE 185

QY 150 IRGISEETTTGVHNLKYMANGILKVPAINVNDSTVTKSKFNLKYGCRSLDGLIKRATDV 209
DB 186 IRGVTEETTTGVHRLYEMHRDGTLLFPAINVNDATVTKSKFDNKYGCGRHSLDGINRATDV 245

QY 210 MIAGKAVVAGYGVGKCAQALRGFGARVIVTEIDPINALQAAMEGYEVTMTDEACQEG 269
DB 246 LIGGKTAVVCGYGVGKCAESLRGQGARVIVTEIDPICALQAAMDGYQVATLDEYVDKA 305

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Db 304 IFITTTGNKDVIRIEHMRDMKMAIIVGNIGHFDNEIQVASLKNHKW-----TNKEQ 355
Qy 325 VDRYRLKNGRRRIILLAEGRVLNLCGAMGHPSPFVMSNSTNQVMAQIELMTHDPKYPGVGH 384
Db 356 VDMIEPNNGRLILLSEGRLLNGLNATGHPSPFVMSASFTNQVLAQIELMTKGDYSNEVY 415
Qy 385 FLPKLDEAVAEAHGLKLVKLTKEKQAOYLGMSCDGPFPKPDHYRY 432
Db 416 ILPKHLDKVARLHLDRIKVLKSLKLNDEQAAYIGVSSEGPFKPEHYRY 463

RESULT 12
Q8FXZ7 PRELIMINARY; PRT; 466 AA.
AC Q8FXZ7 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Adenosylhomocysteinase.
GN AHCY OR BR2097.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.B., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M.J., Shetty J., Malek J., Van Aken S.E.,
RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts."
RL EMBL; AE014496; U.S.A. 99:13148-13153 (2002).
DR EMBL; AE014496; U.S.A. 99:13148-13153 (2002).
DR TIGR; BR2097; -.
KW Complete proteome.
SQ SEQUENCE 466 AA; 50791 MW; 6AB3B4B1C2F0B841 CRC64;

Query Match 57.5%; Score 1305; DB 16; Length 466;
Best Local Similarity 57.4%; Pred. No. 1.1e-91;
Matches 272; Conservative 51; Mismatches 101; Indels 50; Gaps 6;

Qy 1 MSKLPYKVADIGLAAGRWKALDIENEMPGLMRERYASKPLKGARIAGCLHMTVET 60
Db 1 MTASQDFVVKDISLADGWKELDIATETMPGLMAAREEFGKSQLKGARISGLHMTIQT 60
Qy 61 AVLIETLVTLAGVQWSSCNIFSTQNHAAAIAGIPVYAWKGETDEEYLWCIEQTLIF 120
Db 61 AVLIETLKVLAGVRWASCNIFSTQDHAAAIATGTPFAVKGETLEEYWTYTDQIFOW 120
Qy 121 KDG-PLNMILDGGDLTNLIH-----HTKYPQL-----LPG--- 149
Db 121 PDGEPNMLDDGGDATWYLLIGARAEAGEDVLNPSQSEEEVLPQIKRMAATGFFT 180
Qy 150 -----IRGISEETTTGVNHLKYMWANGILKVPAINVNDSTKSKFDNLYGCRSLIDGK 204
Db 181 KQRAAIKGVTEETTTGVNRLYQLKKGLLPFAINVNDSTKSKFDNLYGCRSLVDGIR 240
Qy 205 RATDVMIAKGVAVAGVGDVKGCAQALRGFGARVITTEIDPINALQAAMEGEVVTMD 264
Db 241 RGTDMVMAGKAVVAGVGDVKGKSAQSLAGAGARVKVTEVDPTCALQAAMDGEFVTLDD 300
Qy 265 ACQEGNIFVTTTGCIDIIILGRHFEQKDDAIVCNIGHFDEVIDV-----KWLNAVEK 318
Db 301 AASTADIVTTTGNKDVITTDHMRKDKMCIKDVGNIGHFDNEIQVASLKNHKW----- 352
Qy 319 VNIKPOVDYRLKNGRRRIILLAEGRVLNLCGAMGHPSPFVMSNSTNQVMAQIELMTHDPK 378
Db 319 VNIKPOVDYRLKNGRRRIILLAEGRVLNLCGAMGHPSPFVMSNSTNQVMAQIELMTHDPK 378
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Db 353 TNVKSQVDLIEPDPGKRLLILSEGRLLNGLNATGHPSPFVMSASFTNQVLAQIELMTRTDA 412
Qy 379 YPVGVHFLPKLDEAVAEAHGLKLVKLTKEKQAOYLGMSCDGPFPKPDHYRY 432
Db 413 YKNEVTVLPKHLDEKVARLHLDKLGAKLTVLSEQAAYIGVTPQSPFPKSEHYRY 466

RESULT 13
Q8LE20 PRELIMINARY; PRT; 485 AA.
AC Q8LE20 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Adenosylhomocysteinase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsie.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.B.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation."
RL Genome Biol. 0:0-0 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY085669; AAM62888.1; -.
DR InterPro; IPR000043; Ado_hcyase.
DR Pfam; PF00670; AdoHcyase; 1.
DR TIGRFAMs; TIGR00936; ahcy; 1.
DR PROSITE; PS00738; ADOHCYASE_1; 1.
DR PROSITE; PS00739; ADOHCYASE_2; 1.
SQ SEQUENCE 485 AA; 53401 MW; 11132BBC1F46C86C CRC64;

Query Match 56.8%; Score 1291; DB 10; Length 485;
Best Local Similarity 56.3%; Pred. No. 1.4e-90;
Matches 267; Conservative 54; Mismatches 103; Indels 50; Gaps 6;

Qy 7 YKVADIGLAAGRWKALDIENEMPGLMRERYASKPLKGARIAGCLHMTVETAVLIET 66
Db 14 YKVQMSQADFGRLELEAEVEMPGLMACRTBFGSPQPPKGARITGSLHMTITQTAVLIET 73
Qy 67 LVTLAGVQWSSCNIFSTQNHAAAIAGIPVYAWKGETDEEYLWCIEQTLIF 125
Db 74 LTALGAENVWCSNIFSTQDHAAAIARDSAAPFAWKGETLQEYVWCTERALDWGPGGP 133
Qy 126 NMILDGGDLTNLIH-----HTKYPQL-----LPG--- 149
Db 134 DLIVDDGGDATWYLLIGARAEAGEDVLNPSQSEEEVLPQIKRMAATGFFT 193
Qy 145 QLLPGIRGISEETTTGVNHLKYMWANGILKVPAINVNDSTKSKFDNLYGCRSLIDGK 204
Db 194 KMKRLVGVSEETTTGVNRLYQLKKGLLPFAINVNDSTKSKFDNLYGCRSLPDGLM 253
Qy 205 RATDVMIAKGVAVAGVGDVKGCAQALRGFGARVITTEIDPINALQAAMEGEVVTMD 264
Db 254 RATDVMIAKGVAVAGVGDVKGKSAQSLAGAGARVKVTEVDPTCALQAAMDGEFVTLDD 313
Qy 265 ACQEGNIFVTTTGCIDIIILGRHFEQKDDAIVCNIGHFDEVIDV-----KWLNAVEK 318
Db 314 VVSEADIVTTTGNKDVITTDHMRKDKMCIKDVGNIGHFDNEIQVASLKNHKW----- 373
Qy 324 QVDRY-----RLKNGRRIILLAEGRVLNLCGAMGHPSPFVMSNSTNQVMAQIELMTHDPK 378
Db 374 QVDRY-----RLKNGRRIILLAEGRVLNLCGAMGHPSPFVMSNSTNQVMAQIELMTHDPK 378
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QY 379 YPVGVLFLPKLDEAVAEHLGLKLVNKLTKLTKAQVGLGMSCDGPFKPDHYRY 432
 Db 432 YEKVYVLPKHLDEKVALHGLKGLCARLTKLSDQDYVSIPIEGYKPKPHRY 485

RESULT 14
 Q94929 PRELIMINARY; PRT; 485 AA.
 AC Q94929
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Putative S-adenosyl L-homocysteine hydrolase (EC 3.3.1.1)
 DE (Adenosylhomocysteinase) (S-adenosyl-L-homocysteine hydrolase)
 DE (AdhCysase).
 GN MY9.16.

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopses.
 OX NCBI_TaxID=3702;
 RN [1]

SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
 RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Kosema E., Lam B.,
 RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene MY9.16 (GI:9293955)".
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: ADENOSYLHOMOCYSTEINE IS A COMPETITIVE INHIBITOR OF S-
 ADENOSYL-L-METHIONINE-DEPENDENT METHYL TRANSFERASE REACTIONS;
 CC THEREFORE ADENOSYLHOMOCYSTEINASE MAY PLAY A KEY ROLE IN THE
 CC CONTROL OF METHYLATIONS VIA REGULATION OF THE INTRACELLULAR
 CC CONCENTRATION OF ADENOSYLHOMOCYSTEINE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-HOMOCYSTEINE + H(2)O = ADENOSINE
 CC + L-HOMOCYSTEINE.
 CC -1- COFACTOR: NAD (BY SIMILARITY).
 CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
 CC -1- SIMILARITY: BELONGS TO THE ADENOSYLHOMOCYSTEINASE FAMILY.
 DR EMBL; AY050783; AAK92718.1; -.
 DR InterPro; IPR000043; Ado_hcysase.
 DR Pfam; PF00670; AdhCysase; 1.
 DR TIGRFAMs; TIGR00936; ahcy; 1.
 DR PROSITE; PS00738; ADHCYASE_1; 1.
 DR PROSITE; PS00739; ADHCYASE_2; 1.
 KW Hydrolase; NAD; One-carbon metabolism.
 SQ SEQUENCE 485 AA; 53178 MW; 876079F4782FE532 CRC64;

Query Match 56.2%; Score 1277; DB 10; Length 485;
 Best Local Similarity 55.5%; Pred. No. 1.6e-89;
 Matches 262; Conservative 58; Mismatches 106; Indels 46; Gaps 5;

QY 7 YKVADIGLAAGKRALDIAENEMPGLMRMERYASAKPLKGARIAGCLHMTVETAVLIET 66
 Db 14 YKVDMSQADFGLELEIAEVEPGVSCVTEFGPSQPLKGARITGSLHMTIQTAVLIET 73

QY 67 LVTGAEVQWSSCNIFSTQNHAAAIKAGIPVYAWKGTDBEYLWCIEQTL-YFKDGPL 125
 Db 74 LTALGAEVRWCSCNIFSTQDHAAAIARDAAVFAWKGTLOEYWWCTERALDWDGPGGP 133

QY 126 NMILDGGDLTLNLIH-----TKYP 144
 Db 134 DLIVDDGGDATTLLIHGKVAEIRFAKNGTFDPDPTSTNDNPEFQIVLSIIKDGQLVDPKKYH 193

QY 145 QLLPGIRGISSETTGVHNLKYMANGILKVPAINVNDVSTKSKFDNLYGCRSLIDGK 204
 Db 194 KMKERLVGVSSEETTVGVKRLYQMGTGALLFPAINVNDVSTKSKFDNLYGCRSLPDGLM 253

QY 205 RATDVMIAKVAVAGYGDVGKGAQALRGFGARVIITEIDPINALQAAMEGYEVTWDE 264

Db 254 RATDVMIAKVAVICGYDVGKGAAMKTAGARVITVEIDPICALQALMEGLQVLTLED 313
 QY 265 ACQENIFVTTCGIDIIILGRHFEOMKDDAIVCNIGHFDEIVDKWLN-NAVEKVNIPK 323
 Db 314 VVSEADIFCTTCNKDIIIMVDMHRMKNNAIVCNIGHFDEIMDLGLETPYGVKRTIKP 373

QY 324 QVDRYRLKN-GRRIILLAEGRVLNIGCAMGHSPFVMSNSFTNOVMAQIELWTHPD--KYP 380
 Db 374 QDRWVFPDNTSGIIVLAEGRLNMGICATGHSPFVMSCSFTNOVIAQLELWNEKSSGKYE 433

QY 381 VGVHLEPKKLDEAVAEHLGLKLVNKLTKLTKAQVGLGMSCDGPFKPDHYRY 432
 Db 434 KKVYVLPKHLDEKVALHGLKGLCARLTKLSDQDYVSIPIEGYKPKPHRY 485

RESULT 15
 Q8LPS8 PRELIMINARY; PRT; 485 AA.
 AC Q8LPS8
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE AT3G23810/MY9 15.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopses.
 OX NCBI_TaxID=3702;
 RN [1]

SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY094404; AAM19782.1; -.
 DR InterPro; IPR000043; Ado_hcysase.
 DR Pfam; PF00670; AdhCysase; 1.
 DR TIGRFAMs; TIGR00936; ahcy; 1.
 DR PROSITE; PS00738; ADHCYASE_1; 1.
 DR PROSITE; PS00739; ADHCYASE_2; 1.
 SQ SEQUENCE 485 AA; 53101 MW; 14275615D0996059 CRC64;

Query Match 56.1%; Score 1274; DB 10; Length 485;
 Best Local Similarity 55.5%; Pred. No. 2.8e-89;
 Matches 262; Conservative 57; Mismatches 107; Indels 46; Gaps 5;

QY 7 YKVADIGLAAGKRALDIAENEMPGLMRMERYASAKPLKGARIAGCLHMTVETAVLIET 66
 Db 14 YKVDMSQADFGLELEIAEVEPGVSCVTEFGPSQPLKGARITGSLHMTIQTAVLIET 73

QY 67 LVTGAEVQWSSCNIFSTQNHAAAIKAGIPVYAWKGTDBEYLWCIEQTL-YFKDGPL 125
 Db 74 LTALGAEVRWCSCNIFSTQDHAAAIARDAAVFAWKGTLOEYWWCTERALDWDGPGGP 133

QY 126 NMILDGGDLTLNLIH-----TKYP 144
 Db 134 DLIVDDGGDATTLLIHGKVAEIRFAKNGTFDPDPTSTNDNPEFQIVLSIIKDGQLVDPKKYH 193

QY 145 QLLPGIRGISSETTGVHNLKYMANGILKVPAINVNDVSTKSKFDNLYGCRSLIDGK 204
 Db 194 KMKERLVGVSSEETTVGVKRLYQMGTGALLFPAINVNDVSTKSKFDNLYGCRSLPDGLM 253

QY 205 RATDVMIAKVAVAGYGDVGKGAQALRGFGARVIITEIDPINALQAAMEGYEVTWDE 264
 Db 254 RATDVMIAKVAVICGYDVGKGAAMKTAGARVITVEIDPICALQALMEGLQVLTLED 313

QY	265	ACOEGRIFVTTTCIDIIILGRHFEQMKDDAIVCNIGHFDEIDVKWLN-NAVEKYNIXP	323
Db	314	VVSEADIFCTTTGNKDIIIMVDHMRKKNNAIVCNIGHFONEIDMLGLETPGVKRTIKP	373
QY	324	QVDRYRLKN-GREIILLAEGRLVNLGCAMGHPSFVMSNSFTNOVMAQIELWTHPD--KYP	380
Db	374	QTDRAWVPDTSNGIIVLAEGRLMNLGCATGHPSPVMSCSFTNQVIAQLELWNEKSSGKYE	433
QY	381	GVVHFLPKLDEAVAEAHILGKLVNKLTKTEKQAQYLGMSCDGPPKPDHYRY	432
Db	434	KKYVVLPKHLDERKVAALHLGKLGARLTKUTKQSDYVSIPIVEGPKPVHRY	485

Search completed: December 30, 2003, 10:42:00
Job time : 44 secs

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:37:43 ; Search time 17 Seconds
(without alignments)
1195.032 Million cell updates/sec

Title: US-10-043-787-1
Perfect score: 2271
Sequence: 1 MSDKLPYKVADIGLAAGRK.....QAQYLGMSCDGPFKPDHYRY 432

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2266	99.8	432	1 SAHH_HUMAN	P23526 homo sapien
2	2193	96.6	431	1 SAHH_MOUSE	P50247 mus musculus
3	2194	96.2	431	1 SAHH_RAT	P10760 rattus norv
4	2017.5	88.8	433	1 SAH1_XENLA	P51893 xenopus lae
5	2015.5	88.7	433	1 SAH2_XENLA	P51893 xenopus lae
6	1797	79.1	431	1 SAHH_DROME	Q27580 drosophila
7	1767.5	77.8	432	1 SAHH_ANGOA	O76757 anopheles g
8	1748	77.0	437	1 SAHH_CABEL	P27604 caenorhabdi
9	1733	76.3	433	1 SAHH_SCHPO	O13639 schizosacch
10	1697.5	74.7	430	1 SAHH_DICDI	P10819 dictyosteli
11	1633	71.9	449	1 SAHH_YEAST	P39954 saccharomyc
12	1607.5	70.8	437	1 SAHH_LEIDO	P36889 leishmania
13	1536	67.6	440	1 SAHH_PNECA	Q12663 pneumocysti
14	1516	66.8	471	1 SAHH_CHLTE	Q8kge8 chlorobium
15	1426	62.8	480	1 SAHH_XYFLA	O9pj1 xylella fas
16	1401	61.7	480	1 SAHH_XANCP	Q8pch5 xanthomonas
17	1387	61.1	474	1 SAHH_RALSO	Q8Y387 ralestonia s
18	1386	61.0	480	1 SAHH_XANAC	Q8p84 xanthomonas
19	1373	60.5	485	1 SAHH_STRCO	Q9kmi streptomyce
20	1347.5	59.3	482	1 SAHH_STRAA	Q9366 streptomyce
21	1335.5	58.8	463	1 SAHH_HROSH	O50562 rhodobacter
22	1323.5	58.3	463	1 SAHH_HROCA	P28183 rhodobacter
23	1323	58.3	485	1 SAHH_CATRO	P35007 catharanthu
24	1315.5	57.9	494	1 SAHH_MCTU	O08364 mycobacteri
25	1308	57.6	466	1 SAHH_RHIME	Q92tc1 rhizobium m
26	1306	57.5	485	1 SAHH_PTCR	Q01781 petroselinu
27	1302.5	57.4	492	1 SAHH_MYCLE	Q9ccj4 mycobacteri
28	1302	57.3	466	1 SAHH_BRUME	O8ye49 brucella me
29	1302	57.3	485	1 SAHH_LUPLU	Q9sp37 lupinus lut
30	1299	57.2	466	1 SAHH_AGRTS	Q8u399 agrobacteri
31	1299	57.2	485	1 SAHH_TOBAC	P50248 nicotiana t
32	1296	57.1	466	1 SAHH_RHILO	Q98cm3 rhizobium l
33	1295	57.0	485	1 SAHH_MEDSA	P50246 medicago sa

RESULT 1
SAHH_HUMAN
ID SAHH_HUMAN STANDARD; PRT; 432 AA.
AC P23526; O96A36;
DT 01-NOV-1991 (Rel. 20, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Adenosylhomocysteinease (EC 3.3.1.1) (S-adenosyl-L-homocysteine
DE hydrolase) (AdoHcyase).
GN AHCY OR SAHH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90087640; PubMed=2596825;
RA Coulter-Karis D.E., Herzhfeld M.S.;
RT "Sequence of full length.cdna for human S-adenosylhomocysteine
RT hydrolase.";
RL Ann. Hum. Genet. 53:169-175(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.P., Bates K.N., Bead L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekesch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levesque L.M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.B., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams B.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta, and Skin;
RX MEDLINE=22388257; PubMed=12477932;

ALIGNMENTS

Db 1 MSDKLPYKVADIGLAANGKALDIAENEMPGLMRERYSASKPLKGARIAGCLHMTVET 60
Qy 61 AVLIETVLTGAEVQSSCNIFSTQNHAAATAKAGIPYAWKGETDEEYLWCISQTLF 120
Db 61 AVLIETVLTGAEVQSSCNIFSTQNHAAATAKAGIPYAWKGETDEEYLWCISQTLF 120
Qy 121 KDGPLNMLDDGGDLTNLIHTKYPQLPGIRGISETTTTGVNLYKMMANGILKVPAINV 180
Db 121 KDGPLNMLDDGGDLTNLIHTKYPQLPGIRGISETTTTGVNLYKMMANGILKVPAINV 180
Qy 181 NDSVTKSKFDNLGCGRESLIDGIRATDVMIAGKAVVAGYGVGKCAQALRGFGARVI 240
Db 181 NDSVTKSKFDNLGCGRESLIDGIRATDVMIAGKAVVAGYGVGKCAQALRGFGARVI 240
Qy 241 ITEIDPINALQAAMEGYEVTWDEACQEGNIFVTTTGCIDIIILGRHFEOMKDDAIVCNIG 300
Db 241 ITEIDPINALQAAMEGYEVTWDEACQEGNIFVTTTGCIDIIILGRHFEOMKDDAIVCNIG 300
Qy 301 HFDVEIDVKWLNENAVEKVNIPQVDYRLKNGRRILLAEGLVNLGCMGHPSPVMSN 360
Db 301 HFDVEIDVKWLNENAVEKVNIPQVDYRLKNGRRILLAEGLVNLGCMGHPSPVMSN 360
Qy 361 SFTNQVMAQIELWTHDPKYPVGVHFLPKLDEAVABAHGLKLVNKLTKTEKQAQYLGMS 420
Db 361 SFTNQVMAQIELWTHDPKYPVGVHFLPKLDEAVABAHGLKLVNKLTKTEKQAQYLGMS 420
Qy 421 CDGPPKPDHYRY 432
Db 421 CDGPPKPDHYRY 432

RESULT 2
SAHH MOUSE
ID SAHH MOUSE STANDARD; PRT; 431 AA.
AC P50247; Q91W1; 431 AA.
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Adenosylhomocysteinease (EC 3.1.1.1) (S-adenosyl-L-homocysteine
hydrolase) (AdoHcyase) (Liver copper binding protein) (CUBP).
GN AHCY.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=95386522; PubMed=7657650;
RA Bethin K.E., Petrovic N., Ettinger M.J.;
RT "Identification of a major hepatic copper binding protein as S-
adenosylhomocysteine hydrolase";
RL J. Biol. Chem. 270:20698-20702(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M., Ueding T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: ADENOSYLOHOMOCYSTEINE IS A COMPETITIVE INHIBITOR OF
S-ADENOSYL-L-METHIONINE-DEPENDENT METHYL TRANSFERASE REACTIONS;
THEREFORE ADENOSYLOHOMOCYSTEINASE MAY PLAY A KEY ROLE IN THE
CONTROL OF METHYLATIONS VIA REGULATION OF THE INTRACELLULAR
CONCENTRATION OF ADENOSYLOHOMOCYSTEINE.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine
+ L-homocysteine.
CC -!- COFACTOR: NAD.
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the adenosylhomocysteine family.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; L32836; AAA70378.1; -;
DR EMBL; BC015304; AAH15304.1; -;
DR HSSP; P10760; 1D4F.
DR MGD; MGI:87968; Ahcy.
DR InterPro; IPR000043; Ado_hcyase.
DR Pfam; PF05221; AdoHcyase; 1.
DR Pfam; PF00670; AdoHcyase_NAD; 1.
DR TIGRfam; TIGR00936; ahcy; 1.
DR PROSITE; PS00738; ADHOCYASE_1; 1.
DR PROSITE; PS00739; ADHOCYASE_2; 1.
KW Hydrolase; NAD; One-carbon metabolism.
FT INIT MET 0
FT NP BIND 213 244 NAD (POTENTIAL).
FT CONFLICT 173 173 K -> N (IN REF. 1).
FT SEQUENCE 431 AA; 47557 MW; D577DB2F9D98CA94 CRC64;
SQ
Query Match 96.6%; Score 2193; DB 1; Length 431;
Best Local Similarity 96.8%; Pred. No. 3.8e-157;
Matches 417; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
Qy 2 SDKLPYKVADIGLAANGKALDIAENEMPGLMRERYSASKPLKGARIAGCLHMTVETA 61
Db 1 SDKLPYKVADIGLAANGKALDIAENEMPGLMRERYSASKPLKGARIAGCLHMTVETA 60
Qy 62 VLIETVLTGAEVQSSCNIFSTQNHAAATAKAGIPYAWKGETDEEYLWCISQTLF 121
Db 61 VLIETVLTGAEVQSSCNIFSTQNHAAATAKAGIPYAWKGETDEEYLWCISQTLF 120
Qy 122 DGPLNMLDDGGDLTNLIHTKYPQLPGIRGISETTTTGVNLYKMMANGILKVPAINV 181
Db 121 DGPLNMLDDGGDLTNLIHTKYPQLPGIRGISETTTTGVNLYKMMANGILKVPAINV 180
Qy 182 DSVTKSKFDNLGCGRESLIDGIRATDVMIAGKAVVAGYGVGKCAQALRGFGARVI 241
Db 181 DSVTKSKFDNLGCGRESLIDGIRATDVMIAGKAVVAGYGVGKCAQALRGFGARVI 240
Qy 242 TEIDPINALQAAMEGYEVTWDEACQEGNIFVTTTGCIDIIILGRHFEOMKDDAIVCNIG 301
Db 241 TEIDPINALQAAMEGYEVTWDEACQEGNIFVTTTGCIDIIILGRHFEOMKDDAIVCNIG 300
Qy 302 FVDEIDVKWLNENAVEKVNIPQVDYRLKNGRRILLAEGLVNLGCMGHPSPVMSN 361
Db 301 FVDEIDVKWLNENAVEKVNIPQVDYRLKNGRRILLAEGLVNLGCMGHPSPVMSN 360
Qy 362 FTNQVMAQIELWTHDPKYPVGVHFLPKLDEAVABAHGLKLVNKLTKTEKQAQYLGMS 421
Db 361 FTNQVMAQIELWTHDPKYPVGVHFLPKLDEAVABAHGLKLVNKLTKTEKQAQYLGMS 420

QY 422 DGPFPDHYRY 432
DB 421 NGPFPDHYRY 431

RESULT 3
SAHH RAT STANDARD; PRT; 431 AA.
AC P10760;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl-L-homocysteine
hydrolase) (AdoHcyase).
GN AHCY.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=87118249; PubMed=3027698;
RA Ogawa H., Gomi T., Mueckler M.M., Fujioka M., Backlund P.S. Jr.,
RA Aksanit R.R., Unson C.G., Cantoni G.L.;
RT "Amino acid sequence of S-adenosyl-L-homocysteine hydrolase from rat
liver as derived from the cDNA sequence".
RL Proc. Natl. Acad. Sci. U.S.A. 84:719-723 (1987).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Fischer 344;
RC MEDLINE=95262723; PubMed=7744082;
RA Merta A., Aksanit R.R., Kasir J., Cantoni G.L.;
RT "The gene and pseudogenes of rat S-adenosyl-L-homocysteine
hydrolase".
RL Eur. J. Biochem. 229:575-582 (1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RC TISSUE=Liver;
RX MEDLINE=99315209; PubMed=10387078;
RA Hu Y., Komoto J., Huang Y., Gomi T., Ogawa H., Takata Y., Fujioka M.,
RA Takusagawa F.;
RT "Crystal structure of S-adenosylhomocysteine hydrolase from rat
liver".
RL Biochemistry 38:8323-8333 (1999).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=20493601; PubMed=10913437;
RA Komoto J., Huang Y., Gomi T., Ogawa H., Takata Y., Fujioka M.,
RA Takusagawa F.;
RT "Effects of site-directed mutagenesis on structure and function of
recombinant rat liver S-adenosylhomocysteine hydrolase. Crystal
structure of D244E mutant enzyme".
RL J. Biol. Chem. 275:32147-32156 (2000).
CC -!- FUNCTION: ADENOSYLMOCYSTEINE IS A COMPETITIVE INHIBITOR OF
S-ADENOSYL-L-METHIONINE-DEPENDENT METHYL TRANSFERASE REACTIONS;
THEREFORE ADENOSYLMOCYSTEINASE MAY PLAY A KEY ROLE IN THE
CONTROL OF METHYLATIONS VIA REGULATION OF THE INTRACELLULAR
CONCENTRATION OF ADENOSYLMOCYSTEINE.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine
+ L-homocysteine.
CC -!- COFACTOR: NAD.
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the adenosylhomocysteinase family.

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CC EMBL; M15185; AAA40705.1; -
CC EMBL; U14937; AAA92043.1; -
DR PIR; A26583; A26583.
DR PDB; 1B3R; 23-DEC-98.
DR PDB; 1D4F; 17-JAN-01.
DR PDB; 1D4G; 17-JAN-01.
DR PDB; 1KOU; 17-OCT-01.
DR PDB; 1KY4; 25-SEP-02.
DR PDB; 1KY5; 25-SEP-02.
DR InterPro; IPR000043; Ado hcyase.
DR Pfam; PF05221; AdoHcyase; 1.
DR TIGRfam; TIGR00936; ahcy; 1.
DR PROSITE; PS00738; ADOHCYASE_1; 1.
DR PROSITE; PS00739; ADOHCYASE_2; 1.
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FT INIT MET 0 0
FT NP BIND 213 244 NAD (POTENTIAL).
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FT STRAND 352 428
FT TURN 353 428
SQ SEQUENCE 431 AA; 47407 MW; 537154C9EAA4E380 CRC64;

Query Match
Best Local Similarity 96.2%; Score 2184; DB 1; Length 431;
Matches 415; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 2 SDKLPYKADIGLAANGKRALDIAENMPGLMRERYASAKPLKGARIAGCLHMTVETA 61
DB 1 ADKLPYKADIGLAANGKRALDIAENMPGLMRERYASAKPLKGARIAGCLHMTVETA 60

QY 62 VLTIETLVTLGAEVQWSSCNIFSTQNHAAAAIAKAGIPVYAWKGETDEEYLMWCIETQTLVF 121
DB 61 VLTIETLVTLGAEVQWSSCNIFSTQDHAAAAIAKAGIPVPAWKGETDEEYLMWCIETQTLVF 120

QY 122 DGPLNMLDDGGDLTNLIHTKYPQLLPGRIGISEETTTGVHNLKYMANGILKVPAINVN 181
DB 121 DGPLNMLDDGGDLTNLIHTKYPQLLPGRIGISEETTTGVHNLKYMANGILKVPAINVN 180

QY 182 DSVTKSKFDNLYGCRSLIDGIRATDVMITAGVAVVAGVDGKCAQALRGFGARV 241
DB 181 DSVTKSKFDNLYGCRSLIDGIRATDVMITAGVAVVAGVDGKCAQALRGFGARV 240

QY 242 TEIDPINALQAAMEGYEVTTMTDEACQEGNIFVTTTCGIDIIILGRHPEQMKDDAIVCNIGH 301
DB 241 TEIDPINALQAAMEGYEVTTMTDEACQEGNIFVTTTCGIDIIILGRHPEQMKDDAIVCNIGH 300

QY 302 FDVEIDVKMLNENAVEKVNIPQVDYRLKNGRRRIILAEGRVLNLCGAMGHPSPFVMSNS 361
DB 301 FDVEIDVKMLNENAVEKVNIPQVDYRLKNGRRRIILAEGRVLNLCGAMGHPSPFVMSNS 360

QY 362 FTNQVMAQIELWTHPDKYPVGVHFLPKLDEAVAEHLGKLVNKLTKLTKQAQYLGMS 421
DB 361 FTNQVMAQIELWTHPDKYPVGVHFLPKLDEAVAEHLGKLVNKLTKLTKQAQYLGMS 420

QY 422 DGPFPKPDHYRY 432
DB 421 NGPFPKPDHYRY 431

RESULT 4
SAH1_XENLA
ID -SAH1_XENLA STANDARD; PRT; 433 AA.
AC P51853;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adenosylhomocysteine 1 (EC 3.3.1.1) (S-adenosyl-L-homocysteine
DE hydrolase 1) (ADOHCYASE 1).
GN AHCY1 OR AHCY
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95110290; PubMed=7811234;

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RA Seery L.T., McCabe B.D., Schoenberg D.R., Whitehead A.S.;
RT "S-adenosyl-L-homocysteine hydrolase from Xenopus laevis --
RL Biochem. Biophys. Res. Commun. 205:1539-1546(1994).
CC -|- FUNCTION: ADENOSYLHOMOCYSTEINE IS A COMPETITIVE INHIBITOR OF
CC S-ADENOSYL-L-METHIONINE-DEPENDENT METHYL TRANSFERASE REACTIONS;
CC THEREFORE ADENOSYLHOMOCYSTEINASE MAY PLAY A KEY ROLE IN THE
CC CONTROL OF METHYLATIONS VIA REGULATION OF THE INTRACELLULAR
CC CONCENTRATION OF ADENOSYLHOMOCYSTEINE (BY SIMILARITY).
CC -|- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine
CC + L-homocysteine.
CC -|- COFACTOR: NAD (BY SIMILARITY).
CC -|- PATHWAY: Activated methyl cycle.
CC -|- SIMILARITY: Belongs to the adenosylhomocysteine family.
CC
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CC
CC EMBL; L35559; AAA65963.1; -
DR PIR; JC2480; JC2480.
DR HSSP; P10760; 1D4F.
DR InterPro; IPR000043; Ado_hcyase.
DR Pfam; PF05221; AdoHcyase_1.
DR Pfam; PF00870; AdoHcyase_NAD; 1.
DR TIGRPFAM; TIGR00936; ahcY; 1.
DR PROSITE; PS00738; ADOHCYASE_1; 1.
DR PROSITE; PS00739; ADOHCYASE_2; 1.
KW Hydrolase; NAD; One-carbon metabolism.
FT NP BIND 215 246 NAD (POTENTIAL).
SQ SEQUENCE 433 AA; 47747 MW; 28C7DB273199F2FA CRC64;

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Query Match 88.8%; Score 2017.5; DB 1; Length 433;
Best Local Similarity 87.8%; Pred. No. 5.6e-144;
Matches 380; Conservative 28; Mismatches 24; Indels 1; Gaps 1;

QY 1 MSDKLPYKADIGLAANGKRALDIAENMPGLMRERYASAKPLKGARIAGCLHMTVET 60
DB 1 MSDKLSYKADISLADWGRKAIEIAENEMPGMLKMRHSESKPLKGARIAGCLHMTLQT 60

QY 61 AVLTIETLVTLGAEVQWSSCNIFSTQNHAAAAIAKAGIPVYAWKGETDEEYLMWCIETQTLVF 120
DB 61 AVLTIETLVTLGAEVQWSSCNIFSTQDHAAAAIAKAGIPVYAWKGETDEEYLMWCIETQTLVF 120

QY 121 KDG-PLNMLDDGGDLTNLIHTKYPQLLPGRIGISEETTTGVHNLKYMANGILKVPAIN 179
DB 121 KDGKPLNMLDDGGDLTNLVHNSKYPLLKNGIKGISEETTTGVHNLKYMANGILKVPAIN 180

QY 180 VNSVTYKSKFDNLYGCRSLIDGIRATDVMITAGVAVVAGVDGKCAQALRGFGARV 239
DB 181 VNSVTYKSKFDNLYGCRSLIDGIRATDVMITAGVAVVAGVDGKCAQALRGFGARV 240

QY 240 IITEIDPINALQAAMEGYEVTTMTDEACQEGNIFVTTTCGIDIIILGRHPEQMKDDAIVCNI 299
DB 241 IITEIDPINALQAAMEGYEVTTMTDEACQEGNIFVTTTCGADIVEGRHPEQMKDDAIVCNI 300

QY 300 GHFDVEIDVKMLNENAVEKVNIPQVDYRLKNGRRRIILAEGRVLNLCGAMGHPSPFVMS 359
DB 301 GHFDVEIDVKMLNENAVEKVNIPQVDYRLKNGRRRIILAEGRVLNLCGAMGHPSPFVMS 360

QY 360 NSFTNQVMAQIELWTHPDKYPVGVHFLPKLDEAVAEHLGKLVNKLTKLTKQAQYLGMS 419
DB 361 NSFTNQVMAQIELWTHPDKYPVGVHFLPKLDEAVAEHLGKLVNKLTKLTKQAQYLGMS 420

QY 420 SCDBGPKPDHYRY 432
DB 421 DKEGFPKPDHYRY 433

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RESULT 5
SAH2 XENLA
ID SAH2 XENLA STANDARD; PRT; 433 AA.
AC Q93477;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adenosylhomocysteine 2 (EC 3.3.1.1) (S-adenosyl-L-homocysteine
DE hydrolase 2) (ADHCYASE 2).
GN AHCY2 OR SAHH.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Radomski N., Plessmann U., Mohl C., Weber K., Dreyer C.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ADENOSYLHOMOCYSTEINE IS A COMPETITIVE INHIBITOR OF
CC S-ADENOSYL-L-METHYLINE-DEPENDENT METHYL TRANSFERASE REACTIONS;
CC THEREFORE ADENOSYLHOMOCYSTEINASE MAY PLAY A KEY ROLE IN THE
CC CONTROL OF METHYLATIONS VIA REGULATION OF THE INTRACELLULAR
CC CONCENTRATION OF ADENOSYLHOMOCYSTEINE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine
CC + L-homocysteine.
CC -!- COFACTOR: NAD (BY SIMILARITY).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the adenosylhomocysteine family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ007835; CAA07706.1; -.
DR HSSP; P10760; 1D4F.
DR InterPro; IPR000043; Ado_hcyase.
DR Pfam; PF05221; AdoHcyase_1.
DR Pfam; PF00670; AdoHcyase_NAD; 1.
DR TIGRfam; TIGR00936; ahcY; 1.
DR PROSITE; PS00738; ADHCYASE_1; 1.
DR PROSITE; PS00739; ADHCYASE_2; 1.
DR Hydrolase; NAD; One-carbon metabolism.
FT NP BIND 215 246 NAD (POTENTIAL).
SQ SEQUENCE 433 AA; 47745 MW; 3CB91D67C555B47C CRC64;

Query Match 98.7%; Score 2015.5; DB 1; Length 433;
Best Local Similarity 87.3%; Pred. No. 7.9e-144;
Matches 378; Conservative 29; Mismatches 25; Indels 1; Gaps 1;

QY 1 MSDKLPYKADTGLAAGWKALDIAENPGLMWEERYASKPLKGARIAGLHMTVT 60
DB 1 MSDKLSYKADISLADWGRKAEIAENPGLMKKREMYSESKPLKGARIAGLHMTLT 60
QY 61 AVLIETLVLTGAEVQWSSCNIFSTQNHAAAAAKAGIPVYAWKGETDEEYLWCIEOTLYF 120
DB 61 AVLIETLTGAIEVQWSSCNIFSTQDHAATAKTGVPVYAWKGETDEEYIWCIEGTIYF 120
QY 121 KQG-PLNMILDGGDLTNLIHTKYPOLLPGIRGISETTTGVVHNLKYMANGILKVPALN 179
DB 121 KDGKPLNMLDGGDLTNLVHTKYPOLLKIGKIGISETTTGVVHNLKMKSSGTLQVPALN 180
QY 180 VNSDVTKSFNLYGCRSLIDGKIKATDVMTAGVAVAGYCDVCKGCAQALRGFGARV 239
DB 181 VNSDVTKSFNLYGCRSLIDGKIKATDVMTAGVAVAGYCDVCKGCAQALRGFGARV 240
QY 240 IITEIDPINALQAAMEGYEVTTMDEACQEGNIFVTTCGIDILGRHFQMKDDAIVCNI 299

RESULT 6
SAHH DROME
ID SAHH DROME STANDARD; PRT; 431 AA.
AC Q27580;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adenosylhomocysteine (EC 3.3.1.1) (S-adenosyl-L-homocysteine
DE hydrolase) (AdoHcyase).
GN AHCY13 OR AHCY.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97188525; PubMed=90371110;
RA Caggese C., Ragone G., Barsanti P., Moschetti R., Messina A.,
RA Massari S., Caizzi R.;
RT "The S-adenosyl-L-homocysteine hydrolase of Drosophila melanogaster:
RT identification, deduced amino acid sequence and cytological
RT localization of the structural gene.";
RL Mol. Gen. Genet. 253:492-498(1997).
CC -!- FUNCTION: ADENOSYLHOMOCYSTEINE IS A COMPETITIVE INHIBITOR OF
CC S-ADENOSYL-L-METHYLINE-DEPENDENT METHYL TRANSFERASE REACTIONS;
CC THEREFORE ADENOSYLHOMOCYSTEINASE MAY PLAY A KEY ROLE IN THE
CC CONTROL OF METHYLATIONS VIA REGULATION OF THE INTRACELLULAR
CC CONCENTRATION OF ADENOSYLHOMOCYSTEINE.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine
CC + L-homocysteine.
CC -!- COFACTOR: NAD (BY SIMILARITY).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the adenosylhomocysteine family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X95636; CAA64892.1; -.
DR HSSP; P10760; 1B3R.
DR FlyBase; FBgn0014455; Ahcy13.
DR InterPro; IPR000043; Ado_hcyase.
DR Pfam; PF05221; AdoHcyase; 1.
DR Pfam; PF00670; AdoHcyase_NAD; 1.
DR TIGRfam; TIGR00936; ahcY; 1.
DR PROSITE; PS00738; ADHCYASE_1; 1.
DR PROSITE; PS00739; ADHCYASE_2; 1.
DR Hydrolase; NAD; One-carbon metabolism.
KW NP_BIND 214 245 NAD (POTENTIAL).
SQ SEQUENCE 431 AA; 47252 MW; F083FAA7DF2D898A CRC64;

Query Match 79.1%; Score 1797; DB 1; Length 431;
```


Best Local Similarity 80.2%; Pred. No. 1.9e-127;
Matches 345; Conservative 27; Mismatches 56; Indels 2; Gaps 2;

QY 4 KLPYKADIGLAAGKALDIENEMPGIMRMRRYSASKPLKGIAGLHMTVETAVL 63
Db 3 KPSYKADISLAEGWKALIIAENEMPGIMACRKYGPKLKGARITGCLHMTVQTAVL 62
QY 64 IETLVTLGAQVQWSSCNIFSTQNHAAAIKAGIPVYAWKGETDEEYLWCIBQTLVFKDG 123
Db 63 IETLVTLGAQVQWSSCNIFSTQNHAAAIKAGIPVYAWKGETDEEYMWCIQTLLVFPDG 122
QY 124 -PLNMILDDGGDLTNLIHTKYPQLLPGIRGISETTTGVHNLKYMANGILKVPAINVND 182
Db 123 QPLNMILDDGGDLTNLVHKEFKFQFLKNIKGLSETTTGVHNLKYMFKGRLGVPAINVND 182
QY 183 SVTKSKFNLGCRSLIDGIRKATDVMIAAGVAVVAGVGVGKCAQALRGFGARVIT 242
Db 183 SVTKSKFNLGCRSLIDGIRKATDVMIAAGVAVVAGVGVGKCAQALRGFGARVIT 242
QY 243 EIDPINALQAAMEGYEVTTMDEACOEENIFVTTTGCIDIIILGRHFEQMKDDAIVCNIGHF 302
Db 243 EVDPINALQAAMEGYEVTTMDEACOEENIFVTTTGCIDIIILGRHFEQMKDDAIVCNIGHF 302
QY 303 DVEIDVKLNENAVEKVNKPKQVDYRLKNGRRIILLAEGRVLNLCGAMGHPSPFVMSNSF 362
Db 303 DIEIDVNLNENAVEKVNKPKQVDYRLKNGRRIILLAEGRVLNLCGAMGHPSPFVMSNSF 362
QY 363 TNQVNAQIELWTHPKDPYGVGHFLPKLDEVAEVAHLGKLNKVLTKLTKEQAOYLGMSCD 422
Db 363 TNQVNAQIELWTHPKDPYGVGHFLPKLDEVAEVAHLGKLNKVLTKLTKEQAOYLGMSCD 422
QY 423 GPFKPDHYRY 432
Db 422 GPFKPDHYRY 431

RESULT 7
SAHH ANOGA
ID SAHH ANOGA STANDARD; PRT; 432 AA.
AC O76757;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase).
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G3,
RA Zhao Y., Lu W., Eggleston P.;
RL "The S-adenosyl-L-homocysteine hydrolase of Anopheles gambiae.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ADENOSYLHOMOCYSTEINE IS A COMPETITIVE INHIBITOR OF S-ADENOSYL-L-METHIONINE-DEPENDENT METHYL TRANSFERASE REACTIONS; THEREFORE ADENOSYLHOMOCYSTEINASE MAY PLAY A KEY ROLE IN THE CONTROL OF METHYLATIONS VIA REGULATION OF THE INTRACELLULAR CONCENTRATION OF ADENOSYLHOMOCYSTEINE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine + L-homocysteine.
CC -!- COFACTOR: NAD (BY SIMILARITY).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the adenosylhomocysteinase family.

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CC EMBL; AF080546; AAC29475.1; -;
DR HSSP; P10760; 1D4P.
DR InterPro; IPR000043; Ado hcyase.
DR Pfam; PF05221; AdoHcyase_1.
DR Pfam; PF00670; AdoHcyase_NAD; 1.
DR TIGRfam; TIGR00936; ahcy; 1.
DR PROSITE; PS00738; ADHOCYASE_1; 1.
DR PROSITE; PS00739; ADHOCYASE_2; 1.
KW Hydrolase; NAD; One-carbon metabolism.
FT NP_BIND 214 245
SQ SEQUENCE 432 AA; 47741 MW; B3401186D41A3C66 CRC64;
Query Match 77.8%; Score 1767.5; DB 1; Length 432;
Best Local Similarity 77.7%; Pred. No. 3.1e-125;
Matches 334; Conservative 39; Mismatches 56; Indels 1; Gaps 1;

QY 4 KLPYKADIGLAAGKALDIENEMPGIMRMRRYSASKPLKGIAGLHMTVETAVL 63
Db 3 KPSYKADISLAEGWKALIIAENEMPGIMACRKYGPKLKGARITGCLHMTVQTAVL 62
QY 64 IETLVTLGAQVQWSSCNIFSTQNHAAAIKAGIPVYAWKGETDEEYLWCIBQTLVFKDG 123
Db 63 IETLVTLGAQVQWSSCNIFSTQNHAAAIKAGIPVYAWKGETDEEYMWCIQTLLVFPDG 122
QY 124 -PLNMILDDGGDLTNLIHTKYPQLLPGIRGISETTTGVHNLKYMANGILKVPAINVND 182
Db 123 QPLNMILDDGGDLTNLVHAEHPPELLKEIRGLSETTTGVHNLKYMFGRLGMPAINVND 182
QY 183 SVTKSKFNLGCRSLIDGIRKATDVMIAAGVAVVAGVGVGKCAQALRGFGARVIT 242
Db 183 SVTKSKFNLGCRSLIDGIRKATDVMIAAGVAVVAGVGVGKCAQALRGFGARVIT 242
QY 243 EIDPINALQAAMEGYEVTTMDEACOEENIFVTTTGCIDIIILGRHFEQMKDDAIVCNIGHF 302
Db 243 EIDPINALQAAMEGYEVTTMDEACOEENIFVTTTGCIDIIILGRHFEQMKDDAIVCNIGHF 302
QY 303 DVEIDVKLNENAVEKVNKPKQVDYRLKNGRRIILLAEGRVLNLCGAMGHPSPFVMSNSF 362
Db 303 DCEINVTWLNENAVEKVNKPKQVDYRLNLANGHIIILLAEGRVLNLCGAMGHPSPFVMSNSF 362
QY 363 TNQVNAQIELWTHPKDPYGVGHFLPKLDEVAEVAHLGKLNKVLTKLTKEQAOYLGMSCD 422
Db 363 TNQVNAQIELWTHPKDPYGVGHFLPKLDEVAEVAHLGKLNKVLTKLTKEQAOYLGMSCD 422
QY 423 GPFKPDHYRY 432
Db 423 GPFKPDHYRY 432

RESULT 8
SAHH CAEEL
ID SAHH CAEEL STANDARD; PRT; 437 AA.
AC P27604;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase).
GN DPY-14 OR AHH OR K02F2.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93209535; PubMed=8458573;
RA Prasad S.S., Starr T., Rose A.M.;
RT "Molecular characterization in the dpy-14 region identifies the adenosylhomocysteine hydrolase gene in Caenorhabditis elegans.";
RL Genome 36:57-65 (1993).
RN [2]
RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;
RA Maggi L., Goela D.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ADENOSYLHOMOCYSTEINE IS A COMPETITIVE INHIBITOR OF
CC S-ADENOSYL-L-METHIONINE-DEPENDENT METHYL TRANSFERASE REACTIONS;
CC THEREFORE ADENOSYLHOMOCYSTEINASE MAY PLAY A KEY ROLE IN THE
CC CONTROL OF METHYLATIONS VIA REGULATION OF THE INTRACELLULAR
CC CONCENTRATION OF ADENOSYLHOMOCYSTEINE.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine
CC + L-homocysteine.
CC -!- COFACTOR: NAD.
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SUBUNIT: Homotetramer.
CC -!- SIMILARITY: Belongs to the adenosylhomocysteinase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M64306; AAA28062.1; -;
CC EMBL; S57284; AAB25906.1; -;
CC EMBL; AF043699; AAB97565.1; -;
CC PIR; T32918; T32918.
CC HSSP; P10760; ID4F.
CC WormPep; K02F2.2; CE17154.
CC InterPro; IPR000043; Ado_hcyase.
CC Pfam; PF05221; AdoHcyase; 1.
CC Pfam; PF00670; AdoHcyase_NAD; 1.
CC TIGRfam; TIGR00936; ahcy_1.
CC PROSITE; PS00738; ADHCYASE_1; 1.
CC PROSITE; PS00739; ADHCYASE_2; 1.
CC KJ Hydrolyase; NAD; One-carbon metabolism.
CC FT NP BIND 216 247 NAD (POTENTIAL).
CC SQ SEQUENCE 437 AA; 47535 MW; 53ADAB24507CFCD6 CRC64;

Query Match 77.0%; Score 1748; DB 1; Length 437;
Best Local Similarity 76.7%; Pred. No. 9.3e-124;
Matches 332; Conservative 41; Mismatches 56; Indels 4; Gaps 2;

QY 4 KLPYKVDADIGLAAGWKALDIAENPGLMRWEERYASAKPLKAGRIAGLHMTVETAVL 63
DB 5 KPAVKVADIKLADFGKREILAEENPGLMAMSKTGPSPQLKAGRIAGLHMTIQTAVL 64
QY 64 IETLVLTGAEVQWSSCNIFSTQNHAAAIATAKAGIPVYANKGETDEBYLWCIEQTLVFKDG 123
DB 65 IETLTALGAEVQWSSCNIFSTQDHAAAIATAQTGVPVYANKGETDEBYEWCIEQTLVFKDG 124
QY 124 -PLNMLDGGDLTNLHVKYQPLLPGIRGISSETTTGVHNLKYMANGILKVPAINVD 182
DB 125 QPLNMLDGGDLTNLHVKYQPLLPGIRGISSETTTGVHNLAKMLAKGDLKVPAINVD 184
QY 183 SVTKSKFDNLGYCRESLIDGIKRATDVMTAGVAVVAGYGVKGCQAALRGFGARVIT 242
DB 185 SVTKSKFDNLGYRESLPGIKRATDVMTAGVAVVAGYGVKGCQAALRGFGARVIT 244
QY 243 EIDPINALQAAMEGYVTMTDEACQEGNIFVTTCGIDILGRHFPMQKDDAIVCNIGHF 302
DB 245 EIDPINALQAAMEGYVTMTLEEAAPKANIIVTTGCKDIVTGKHFELLPNDALVCNVGHF 304
QY 303 DVEIDVKWLNENAVEKNIKPQVDRLKNGRRIILAEGLVNLGCAMGHPSPFVMSNSF 362
DB 305 DCEIDVKWLNATKDDTIKQVDRLKNGRRIILAEGLVNLGCATGHPSPFVMSNSF 364
QY 363 TNQVMAQIELWTH---PDKYPGVGHFLPKKLDEAAVEAHGLKLVNKLTKLTKQAOYLGM 419
DB 365 TNQVLQVLELWTKFGTPQYKGLVLPKTLDEEVAYLHLAQGLVNLKLSDEQASYLGV 424
QY 420 SCGGPKPDHRY 432
||:|||||

Db 425 PVAGPKPDHRY 437

RESULT 9
SAHH_SCHPO
ID SAHH_SCHPO STANDARD; PRT; 433 AA.
AC O13639;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl-L-homocysteine
DE hydrolase) (AdoHcyase).
GN SPBC8D2.18C OR P1047.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetaceae;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=20089027; PubMed=10620777;
RA Machida M., Yamazaki S., Kunihiro S., Tanaka T., Kushida N., Jinno K.,
RA Haikawa Y., Yamazaki J., Yamamoto S., Sekine M., Oguchi A., Nagai Y.,
RA Sakai M., Aoki K., Ogura K., Kudoh Y., Kikuchi H., Zhang M.Q.,
RA Yanagida M.;
RT "A 38 kb segment containing the cdc2 gene from the left arm of fission
RT yeast chromosome II: sequence analysis and characterization of the
RT genomic DNA and cDNAs encoded on the segment.";
RL Yeast 16:71-80(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine
CC + L-homocysteine.
CC -!- COFACTOR: NAD.
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the adenosylhomocysteinase family.
CC -----
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CC -----

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CC -----
DR EMBL; AB004537; BAA21427.1; -.
DR EMBL; AL022072; CAA17833.1; -.
DR PIR; T40763; T40763.
DR HSSP; P10760; 183R.
DR GeneDB_Spombe; SPBC8D2.18c; -.
DR InterPro; IPR000043; Ado_hcyase.
DR Pfam; PF05221; AdoHcyase; 1.
DR Pfam; PF00670; AdoHcyase_NAD; 1.
DR TIGRFAMs; TIGR00936; ahcy; 1.
DR PROSITE; PS00738; ADHCYASE_1; 1.
DR PROSITE; PS00739; ADHCYASE_2; 1.
KW hydrolase; NAD; One-carbon metabolism.
FT NP_BIND 215 246 NAD (POTENTIAL).
SQ SEQUENCE 433 AA; 47383 MW; 8B4279CC2B518E13 CRC64;

Query Match 76.3%; Score 1733; DB 1; Length 433;
Best Local Similarity 77.8%; Pred. No. 1.2e-122;
Matches 330; Conservative 40; Mismatches 56; Indels 2; Gaps 2;

QY 7 YKVADIGLAAGRKALDIAENEMPGLMRMRYSASKPLKGARIAGCLHMTVETAVLIET 66
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 6 YKVADISLAAGFGRKEIEIAENEMPGLIANREKAKSQPLKGARIAGCLHMTIQTAVLIET 65
QY 67 LVTLAGVQWSSCNIFSTQNHAAAAIAKAGIPYAWKGETDEEYLWCIEQTL-YFKDG-P 124
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 66 LVALGAEVTSWSSCNISTQDHAAAAIAATGVPVFAWKGETEEEYLCIEQQLKSPSGKP 125
QY 125 LNMILDDGDLTLNLIHTKYPQLLPGIRGISEETTTGVHNLKYMANGILKVPAINVDSV 184
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 126 LNMILDDGDLTLNLIHTKYPQLLPGIRGISEETTTGVHNLKYMANGILKVPAINVDSV 185
QY 185 TSKSFNLYGCRSLIDGIRKATDVNLAGVAVVAGVDVGKCAQALRGFGARVLIETI 244
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 186 TSKSFNLYGCRSLIDGIRKATDVNLAGVAVVAGVDVGKCAQALRGFGARVLIETI 245
QY 245 DPINALQAAMEGYEVTTMDEACQEGNI FVTTTCIDIIILGRHFQMKDDAIVCNIGHFDV 304
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 246 DPINALQAAMEGYEVTTMDEACQEGNI FVTTTCIDIIILGRHFQMKDDAIVCNIGHFDV 305
QY 305 EIDVKVNLNENAVEKNIKQVDYRLKNGRRIILLAEGRVLNLCGAMGHPSPFVMSNFTN 364
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 306 EIDVAVLKNANAKVDVNIKPQVDYRLKNGRRIILLAEGRVLNLCGAMGHPSPFVMSNFTN 365
QY 365 QVMAQIELWTHDPKYPGVHFLPKLDEAVABAHGLKLVNKLTKLTKAQYLGMSCDGP 424
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 366 QVLAQIALWTDNTSYPLGVHMLPKLDEEVARHLKGLGVKLTLTLSVQSDYLGIPVDGP 425
QY 425 FKPDHYRY 432
DB :|||||
DB 426 YKADHYRY 433

RESULT 10
SAHH_DICDI
ID SAHH_DICDI STANDARD; PRT; 430 AA.
AC P10819;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adenosylhomocysteinease (EC 3.3.1.1) (S-adenosyl-L-homocysteine
DE hydrolase) (AdoHcyase).
GN SAHA.
OS Dictyostellium discoideum (Slime mold).
OC Eukaryota; Mycotozoa; Dictyostellida; Dictyostellum.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88240426; PubMed=3288206;
RA Kasir J., Aksamit R.R., Backlund P.S. Jr., Cantoni G.L.;
RT "Amino acid sequence of S-adenosyl-L-homocysteine hydrolase from
RT Dictyostellum discoideum as deduced from the cDNA sequence.";
RL Biochem. Biophys. Res. Commun. 153:359-364(1988).

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[2]
RN RP SEQUENCE OF 258-430 FROM N.A.
RX MEDLINE=89000991; PubMed=3139100;
RA Guitton M.C., Part D., Veron M.;
RT "Cloning of a cDNA for the S-adenosyl-L-homocysteine hydrolase from
RT Dictyostellum discoideum.";
RL Biochimie 70:835-840(1988).
CC -1- FUNCTION: ADENOSYLHOMOCYSTEINE IS A COMPETITIVE INHIBITOR OF
CC S-ADENOSYL-L-METHIONINE-DEPENDENT METHYL TRANSFERASE REACTIONS;
CC THEREFORE ADENOSYLHOMOCYSTEINASE MAY PLAY A KEY ROLE IN THE
CC CONTROL OF METHYLATIONS VIA REGULATION OF THE INTRACELLULAR
CC CONCENTRATION OF ADENOSYLHOMOCYSTEINE.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine
CC + L-homocysteine.
CC -1- COFACTOR: NAD.
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotetramer.
CC -1- SIMILARITY: Belongs to the adenosylhomocysteinease family.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M19937; AAA33165.1; -.
DR EMBL; X12523; CAA31040.1; -.
DR PIR; A27655; A27655.
DR HSSP; P10760; 1D4F.
DR DictyDb; D005004; saha.
DR InterPro; IPR000043; Ado_hcyase.
DR InterPro; IPR000205; NAD_binding.
DR Pfam; PF05221; AdoHcyase; 1.
DR Pfam; PF00670; AdoHcyase_NAD; 1.
DR TIGRFAMs; TIGR00936; ahcy; 1.
DR PROSITE; PS00738; ADHCYASE_1; 1.
DR PROSITE; PS00739; ADHCYASE_2; 1.
KW hydrolase; NAD; One-carbon metabolism.
FT NP_BIND 213 244 NAD (POTENTIAL).
FT CONFLICT 258 258 I -> V (IN REF. 2).
FT CONFLICT 261 265 METAA -> KSSPWKP (IN REF. 2).
FT CONFLICT 268 269 SN -> HYQT (IN REF. 2).
FT CONFLICT 312 312 A -> G (IN REF. 2).
FT CONFLICT 324 324 D -> S (IN REF. 2).
FT CONFLICT 360 364 FCNQT -> SVTK (IN REF. 2).
FT CONFLICT 383 383 L -> P (IN REF. 2).
SQ SEQUENCE 430 AA; 47083 MW; D56DF0F84DE45774 CRC64;

Query Match 74.7%; Score 1697.5; DB 1; Length 430;
Best Local Similarity 74.6%; Pred. No. 5.6e-120;
Matches 320; Conservative 38; Mismatches 70; Indels 1; Gaps 1;

QY 4 KLPYKVDIGLAAGRKALDIAENEMPGLMRMRYSASKPLKGARIAGCLHMTVETAVL 63
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3 KLPYKVDISLAAGFGRKEIEIAENEMPGLMTRKKYGPQALKGARIAGCLHMTIQTAVL 62
QY 64 IETLVTLAGVQWSSCNIFSTQNHAAAAIAKAGIPYAWKGETDEEYLWCIEQTLYFKDG 123
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 63 IETLTALGAQVQWSSCNIFSTQDQAAAAIAATGVPVYAWKGETEEEYNCVQETIVFDG 122
QY 124 PLNMILDDGDLTLNLIHTKYPQLLPGIRGISEETTTGVHNLKYMANGILKVPAINVDS 193
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 123 PLNMILDDGDLTLNLIHTKYPQLLPGIRGISEETTTGVHNLKYMANGILKVPAINVDS 192
QY 184 VTKSKFDNLYGCRSLIDGIRKATDVNLAGVAVVAGVDVGKCAQALRGFGARVLIET 243
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 183 VTKSKFDNLYGCRSLIDGIRKATDVNLAGVAVVAGVDVGKCAQALRGFGARVLIET 242
QY 244 IDPINALQAAMEGYEVTTMDEACQEGNI FVTTTCIDIIILGRHFQMKDDAIVCNIGHFD 303
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 243 IDPINALQAAMEGYEVTTMDEACQEGNI FVTTTCIDIIILGRHFQMKDDAIVCNIGHFD 302

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QY 304 VEIDVKWLNENAVEKVNIPQVDYRLKNGRRITLLAEGRLVNLGCMGHPSPFVMSNST 363
DB 303 CEIDVAWLNANA-KDVTVPQVDYRLANGVHLLAEGRLVNLGCGTGHSPFVMSNSFC 361
QY 364 NQMAQIELWTHDPDKYPVGVHFLPKKLDEAVAHAHLGKLVNLTKLTEKQAQYLGMSCDG 423
DB 362 NOTLAQIALWTKTEEYPLGVHLLPKLIDBEVARLHLDLQAKLTTLTKQSEYLSVPVAG 421
QY 424 PKPDPHYRY 432
DB 422 PYKVDHYRY 430

RESULT 11
SAHH_YEAST
ID SAHH_YEAST STANDARD; PRT; 449 AA.
AC P39954;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Adenosylhomocysteine (EC 3.3.1.1) (S-adenosyl-L-homocysteine
DE hydrolase) (AdoHcyase).
GN SAH1 OR YER043C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX PubMed=9169868;
RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
RA Cherry J.M., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
RA Lin D., Moesdale D., Nakahata K., Namath A., Norgren R., Oefner P.,
RA Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
RL Nature 387:78-81(1997).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine
CC + L-homocysteine.
CC -1- COFACTOR: NAD.
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
CC
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CC
CC EMBL; U18796; AAB64578.1; --
CC PIR; S50546; S50546.
CC HSP; P10760; I3R.
CC SGD; S000845; SAH1.
CC GO; GO:0004013; P:adenosylhomocysteine activity; NAS.
CC GO; GO:0006555; P:methionine metabolism; NAS.
CC GO; GO:0016259; P:selenocysteine metabolism; NAS.
CC InterPro; IPR000043; Ado_hcyase.
CC Pfam; PF05221; AdoHcyase; 1.
CC Pfam; PF00670; AdoHcyase_NAD; 1.
CC TIGRfam; TIGR00936; ahcy; 1.
CC PROSITE; PS00738; ADHOCYASE_1; 1.
CC PROSITE; PS00739; ADHOCYASE_2; 1.
CC Hydrolase; NAD; One-carbon metabolism.
KW NP_BIND 217 248 NAD (POTENTIAL).
SQ SEQUENCE 449 AA; 49125 MW; D98D9DD329374F5B CRC64;

Query Match 71.9%; Score 1633; DB 1; Length 449;

Best Local Similarity 70.8%; Pred. No. 4e-115;
Matches 313; Conservative 52; Mismatches 61; Indels 16; Gaps 3;
QY 7 YKVDIGLAAGRKALDTAENEMPGLMRREYSASKPLKGARIAGCLHMTTAVLIET 66
DB 8 YKIDISLAAGRKELIAEHEMPLMAIRKAYGDVQPLKGARIAGCLHMTTAVLIET 67
QY 67 LVTLAGAEVWSSCNFTSTONHAAAIKAGIPYAWKGTDEEYLWCISOTLY-PKDG-P 124
DB 68 LVALGAETWSSCNYSYTDHAAAIASGVVFAWKGETEEYLCISQQLFAFDNKK 127
QY 125 LNMILDGCGDLTLNHTKYPOLLPGIRGISEETTTGVHNLKYMANGILKVPAINVDSV 184
DB 128 LNLILDGCGDLTLVHEKHPEMLDCFGLSEETTTGVHLYRMVKGKLPAINVDSV 187
QY 185 TKSDFDNLGCRSLIDGIKRATDVMIAGKAVAVAGYGVGKCAQALRGFGARVITETI 244
DB 188 TKSDFDNLGCRSLVDGIKRATDVMLAGKAVAVAGYGVGKCAALRGFGARVITETI 247
QY 245 DPINALQAAMEGYEVTMTDEACQEGNIFVTTTGCIDIIILGRHPEQMKDDAIVCNIGHFDV 304
DB 248 DPINALQAAMEGYQVVTMEDASHIGQVFTTTGCRDIINGEHFINNPEDAIVCNIGHFDI 307
QY 305 EIDVKWLNENAVEKVNIPQVDYRLKNGRRITLLAEGRLVNLGCMGHPSPFVMSNSTN 364
DB 308 EIDVAWLKANAKECINIKPQVDYRLSSGRHVILLANGRLVNLGCGTGHSSPFVMSCSFN 367
QY 365 QVMAQIELWTHDPDK-----YPGVHFLPKKLDEAVAHAHLGKLVNLTKL 410
DB 368 QVLAQIALFKSNDKSFREKHIEFQKTPPEVGVHVLPLKILDEAVAKFHLGRLVLTLS 427
QY 411 EKQAOYLGMSCDGPFKDPHYRY 432
DB 428 KVQSEYLGIPPEGPFADHYRY 449

RESULT 12
SAHH_LEIDO
ID SAHH_LEIDO STANDARD; PRT; 437 AA.
AC P36889;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adenosylhomocysteine (EC 3.3.1.1) (S-adenosyl-L-homocysteine
DE hydrolase) (AdoHcyase).
OS Leishmania donovani.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5661;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DI700;
RX MEDLINE=92365726; PubMed=1501636;
RA Henderson D.M., Hanson S., Allen T., Wilson K., Coulter-Karis D.E.,
RA Greenberg M.L., Hersfield M.S., Ullman B.;
RT "Cloning of the gene encoding Leishmania donovani
RT S-adenosylhomocysteine hydrolase, a potential target for
RT antiparasitic chemotherapy.";
RL Mol. Biochem. Parasitol. 53:169-183(1992).
CC -1- FUNCTION: ADENOSYLHOMOCYSTEINE IS A COMPETITIVE INHIBITOR OF
CC S-ADENOSYL-L-METHIONINE-DEPENDENT METHYL TRANSFERASE REACTIONS;
CC THEREFORE ADENOSYLHOMOCYSTEINASE MAY PLAY A KEY ROLE IN THE
CC CONTROL OF METHYLATIONS VIA REGULATION OF THE INTRACELLULAR
CC CONCENTRATION OF ADENOSYLHOMOCYSTEINE.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine
CC + L-homocysteine.
CC -1- COFACTOR: NAD.
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
CC
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 DR HMBL; M76556; AAA29265.1; -
 DR HSSP; P10760; 1B3R.
 DR InterPro; IPR000043; Ado hcyase.
 DR Pfam; PF05221; AdoHcyase; 1.
 DR Pfam; PF06670; AdoHcyase; NAD; 1.
 DR TIGRfam; TIGR00936; ahcy; 1.
 DR PROSITE; PS00738; ADOHCYASE 1; 1.
 DR PROSITE; PS00739; ADOHCYASE 2; 1.
 KW Hydrolyase; NAD; One-carbon metabolism.
 FT NP_BIND 213 244 NAD (POTENTIAL).
 SQ SEQUENCE 437 AA; 47791 MW; D687C918DE2B0637 CRC64;

Query Match 70.8%; Score 1607.5; DB 1; Length 437;
 Best Local Similarity 70.5%; Pred. No. 3.2e-113;
 Matches 310; Conservative 46; Mismatches 73; Indels 11; Gaps 4;

QY 1 MSKLPYKADVGLAAGKRGKALDIAENEMPGMLMRERYASAKPLKGARIAGCLHMTVET 60
 DB 1 MAD---YKVKDLSLAEWGRKALAEENEMPGMLREYGPSQPLKGAKIAGCLHMTVQT 57
 QY 61 AVLIETLVTLGAEVOWSSCNIFSTONHAAAIAKAGIPVYAWKGETDEEYLWCIEQTLL-- 118
 DB 58 AVLIETLKALGADVRSNCNIFSTONHAAAIAKAGIPVYAWKGETDEEYECIAQTVMG 117
 QY 119 YPKDGLNMLDDGDLTLNHTKYPQLPGIRGISEETTTGVNLYKMMANGILKVPAL 178
 DB 118 PSGDGLNMLDDGDLTLNHTKYPQLPGIRGISEETTTGVNLYKXELSGNLPMCAI 177
 QY 179 NVNDSVTSKFPNLVGCRESLIDGIRKATDVMIAKVAVAGVDVGKCAQALRGFGAR 238
 DB 178 NVNDSVTSKFPNLVGCRESLIDGIRKATDVMIAKVAVAGVDVGKCAQALRAFGAR 237
 QY 239 VIITEIDPINALQAAMEGYEVTTMTDEACQEGNIFVTTTCIDIIILGRHPEQMKDDAIVCN 298
 DB 238 VVTEVDPIALQAAMEGQVALVEDVMADAHIFVTTTGNDDIIITSEHPHRRDDAIVCN 297
 QY 299 IGHFDVEIDVKLENENAVEKVNIPQVDYRRLKNGRRRIILLAEGRVLNLGCGAMGHPFSFM 358
 DB 298 IGHFDTEIQVGLWLEANAKEHVEIKQVDYRTWNGRHIILLAKRVLNLGCGAMGHPFSFM 357
 QY 359 SNSFTNQVMAQIELWTHPD--KYP-----VGVHPLPKLDEAVAEHLGKLVNKLTKLTEK 412
 DB 358 SNSFTNQVLAQIELWNSRNGKYPKDGKAGVFFLPKALDEKVAALHLAHVGAKLTKLTPK 417
 QY 413 QAQYLGMSCDGPFKPDHYRY 432
 DB 418 QAIEYINCPVNGPFKPDHYRY 437

RESULT 13
 ID SAHH_PNECA STANDARD; PRT; 440 AA.
 AC Q1263;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Adenosylhomocysteinease (EC 3.3.1.1) (S-adenosyl-L-homocysteine
 DE hydrolyase) (AdoHcyase) (Fragment).
 GN SAHH.
 OS Pneumocystis carinii.
 OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
 OC Pneumocystis.
 OX NCBI_TaxID=4754;
 RP [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Rattus;
 RX MEDLINE=96420115; PubMed=8822814;

RA Lasbury M.E., Brady S., McLaughlin G., Bartlett M.S., Smith J.W.,
 RA Lee C.H.;
 RT "Cloning of the S-adenosylhomocysteine hydrolase gene of *Pneumocystis*
 RT *carinii*";
 RL J. Eukaryot. Microbiol. 43:68-6S(1996).
 CC -!- FUNCTION: ADENOSYLHOMOCYSTEINE IS A COMPETITIVE INHIBITOR OF
 CC S-ADENOSYL-L-METHIONINE-DEPENDENT METHYL TRANSFERASE REACTIONS;
 CC THEREFORE ADENOSYLHOMOCYSTEINASE MAY PLAY A KEY ROLE IN THE
 CC CONTROL OF METHYLATIONS VIA REGULATION OF THE INTRACELLULAR
 CC CONCENTRATION OF ADENOSYLHOMOCYSTEINE.
 CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine
 CC + L-homocysteine.
 CC -!- COFACTOR: NAD (BY SIMILARITY).
 CC -!- PATHWAY: Activated methyl cycle.
 CC -!- SIMILARITY: Belongs to the adenosylhomocysteinease family.
 CC -----
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 CC EMBL; U57795; AAC98514.1; -
 CC HSSP; P10760; 1B3R.
 DR InterPro; IPR000043; Ado hcyase.
 DR Pfam; PF05221; AdoHcyase; 1.
 DR Pfam; PF06670; AdoHcyase; NAD; 1.
 DR TIGRfam; TIGR00936; ahcy; 1.
 DR PROSITE; PS00738; ADOHCYASE 1; 1.
 DR PROSITE; PS00739; ADOHCYASE 2; 1.
 KW Hydrolyase; NAD; One-carbon metabolism.
 FT NON_TER 1 1
 FT NP_BIND 222 253 NAD (POTENTIAL).
 SQ SEQUENCE 440 AA; 48766 MW; BEF5360C8D9F514D CRC64;

Query Match 67.6%; Score 1536; DB 1; Length 440;
 Best Local Similarity 69.9%; Pred. No. 7.4e-108;
 Matches 306; Conservative 38; Mismatches 72; Indels 22; Gaps 7;

QY 14 LAAGRKALDIAENEMPGMLMRERYASAKPLKGARIAGCLHMTVETAVLIETLVTLGAE 73
 DB 6 LAEWGRKELAEENEMPGMLISCR-RNMRFPKPLR-VQIAGCLHMTIQTAVLIETLVGAE 63
 QY 74 VQWSSCNIFSTONHAAAIAKAGIPVYAWKGETDEEYLWCIE-QTLYFKDGP-LNMILDD 131
 DB 64 VQWSSCNIFSTQDHAAAIAAASGISVPAWKGETEBEYLWCIEQTLTSPKQGRHLMILDD 123
 QY 132 GGDLTNLHTKYPQLPGIRGISEETTTGVNLYKMMANGILKVPAINVDSVTSKFPDN 191
 DB 124 GGDVTSLVNHYKYPDLKNCKGISEETTTGVQFYKMLKEGKLKVPAINVDSVTSKFPDN 183
 QY 192 LYG-----CRESLIDGIRKATDVMIAKVAVAGVDVGKCAQALRGF 235
 DB 184 LYGVSLVLIYKIISNLIKLRCSLIDGIRKATDVMIAKVAIVAGVDVGKCAQALRGF 243
 QY 236 GARVIITEIDPINALQAAMEGYEVTTMTDEACQEGNIFVTTTCIDIIILGRHPEQMKDDAI 295
 DB 244 GARVIITEIDPINALQAAMEGYQVAVMEVADQADIFVTATGCKDIIICERHFEAMKNDAI 303
 QY 296 VCNIGHFDVEIDVKLENENAVEKVNIPQVDYRRLKNGRRRIILLAEGRVLNLGCGAMGHP 355
 DB 304 ICNIGHFDVEIDVAVLWILKKCSISINIKQVDYRRLKNGRRRIILLAEGRVLNLGCGATGHS 363
 QY 356 FVMSNFTNQVMAQIELWTHPD-KYPVGVHPLPKLDEAVAEHLGKLVNKLTKLTEKQA 414
 DB 364 FVMSNFTNQVLAQIALWTAQEGQYPLGVHPLPKLDEAVARHLHLSKLG-KLTSLTPEGS 422
 QY 415 QYLGMSCDGPFKPDHYRY 432
 DB 423 AYLDIPIDGPKYKSEHYRY 440

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RESULT 14
SAHH CHLTE
ID SAHH CHLTE STANDARD; PRT; 471 AA.
AC Q8KEG8;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Adenosylhomocysteinease (EC 3.3.1.1) (S-adenosyl-L-homocysteine
hydrolyase) (AdoHcyase).
GN AHCY OR SAHH OR CT0721.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID=1097;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=TLS / ATCC 49652 / DSM 12025;
RX MEDLINE=22103685; PubMed=12093901;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson E.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine
+ L-homocysteine.
CC -!- COFACTOR: NAD (By similarity).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the adenosylhomocysteinease family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AB012843; AAM71958.1; -
CC TIGR; CT0721; -.
CC HAMAP; MF_00563; -.
CC InterPro; IPR000043; Ado_hcyase.
CC InterPro; IPR000205; NAD_binding.
CC Pfam; PF05221; AdoHcyase_1.
CC Pfam; PF00670; AdoHcyase_NAD; 1.
CC TIGRFAMs; TIGR00936; anc7; 1.
CC PROSITE; PS00738; ADHCYASE_1; 1.
CC PROSITE; PS00739; ADHCYASE_2; 1.
CC KEGG; K01100; AdoHcyase; 1.
CC FT NP BIND 254 285 NAD (POTENTIAL)
CC SEQUENCE 471 AA; 51949 MW; 31B082405D241047 CRC64;
CC
Query Match 66.8%; Score 1516; DB 1; Length 471;
Best Local Similarity 64.2%; Pred. No. 2.6e-106;
Matches 300; Conservative 49; Mismatches 76; Indels 42; Gaps 6;
QY 5 LPYKVADIGLAWGRKALDAENEMGLMWRERYASRPLKAGTAGGLHWTAVLI 64
DB 8 LDYKVADISLAEWGRKEIEIAEKEMPLMATRKXKYEGRKPLAGARTAGSLHWTIQAVLI 67
QY 65 ETLVLTGAEVQVSCNIFSTQNHAAIAAGKIPVYAWKGETDEEYLCIEOTLYPKD-- 122
DB 68 ETLVELGADVWRWASCNIFSTQDHAAIAAAGVVFVWKGETIDETWCTRQILLEPGL 127
QY 123 GPNMLTDGGDLTNLIHTKY-----PQLL----- 147
DB 128 GP-NLIVDDGGDNLMIHFGYKIENDPMDLTKTPGNAEBKALLQLKAVFAEDNQSRHWKV 186

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QY 148 -PGIRGISSETTTGVHNLKYMANGILKVPAINVNDVTKSKFDNLYGCRSLDGIKRA 206
DB 187 AGMKGVSETTTGVHRLYQMKEGELLFPAINVNDVTKSKFDNLYGCRSLADGIKRA 246
QY 207 TDVMIAGKVAVVAGYGDVGKCAQALRGFGARVVIITEIDPINALQAAMEGYEYTTMDEAC 266
DB 247 TDVMIAGKVAVVAGYGDVGKCAHSMRSYGARVIVTEIDPICALQAAMEGFVTTMEEAV 306
QY 267 QEGNIFVTTTGCIDITLGRHFFOMKDDAIVCNIGHFDVDEIDVKWLN-NAVEKNIKPQV 325
DB 307 KEGNIFVTATGNKDVITLDHIKQMRDEAIVCNIGHFDNEIQVDALNNFKGATRNKIPQV 366
QY 326 DRYRLKNGRRIILAEGRVLNLCGAMGHPFSFVMSNSFTNQVMAQIELWTHPDKVPYGVHF 385
DB 367 DRYVFENGNCIYLLAEGRVLNLCGATGHPFSFVMSNSFTNQTLAQIELW--QNDYKGVYR 424
QY 386 LPRKLDVAEVAEHLGKLNKLTLEKQAYQLGMSCDGPKDPDHYRY 432
DB 425 LPRKLDVEARLHLGQIGAKLTLTKEQADYIGVPVEGPKPEHYRY 471
RESULT 15
SAHH XYLFA
ID SAHH XYLFA STANDARD; PRT; 480 AA.
AC Q9PEJ1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adenosylhomocysteinease (EC 3.3.1.1) (S-adenosyl-L-homocysteine
hydrolyase) (AdoHcyase).
GN AHCY OR XF1037.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=9a5C; PubMed=10910347;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hobeisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Leite L.C.C.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins A.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshuko M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine
+ L-homocysteine.
CC -!- COFACTOR: NAD (By similarity).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

```

```
CC -1- SIMILARITY: Belongs to the adenosylhomocysteinase family.
CC -----
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CC -----
DR EMBL: AE003941; AAF83847.1; ALT_INIT.
DR FIR: D82730; D82730.
DR HSP: P10760; I1B3R.
DR HAMAP: MF_00563; -; 1.
DR InterPro: IPR000043; Ado_hcyase.
DR Pfam: PF05221; AdoHcyase_1.
DR Pfam: PF00670; AdoHcyase_NAD; 1.
DR TIGRPFAM: TIGR00936; ancY; 1.
DR PROSITE: PS00738; ADHCYASE_1; 1.
DR PROSITE: PS00739; ADHCYASE_2; 1.
DR Hydrolase; NAD; One-carbon metabolism; Complete proteome.
FW NP BIND 261 292 NAD (POTENTIAL).
SQ SEQUENCE 480 AA; 52936 MW; 272CDFBFB997CA7 CRC64;

Query Match 62.8%; Score 1426; DB 1; Length 480;
Best Local Similarity 61.3%; Pred. No. 1.5e-99;
Matches 287; Conservative 52; Mismatches 87; Indels 42; Gaps 6;

QY 7 YKVADIGLAAGWKALDIAENENPGLMRMRERYASKPLKGARIAGCLHMTVETAVLIET 66
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
13 YKIADISLTDWGRKEIDIAEHMPGLMSIRRYASKQPLKGVRTGSLHMTIQTAVLIET 72
QY |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 LVTGLAEVOWSSCNIFSTONHAAAAAKAGIPVYANKGETDEEYLWCIEOTLVF--KGGP 124
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
73 LKDIGADVWASCNIFSTQDHAATAATSGTPVFAWKGETLEBYWDTCTQALTFTLS DGT 132
QY |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
125 L---NMILDGGDLTNLIHTKY-----PQLL-----PGI--- 150
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
133 LTGPELIVDDGGDATLLIHKGYELENGSTWVDSPLSEEQVIKRLKRIATIERPGYWR 192
QY |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 -----RGISEETTTGVNLYKMWANGILKVPAINVDSVTKSKFDNLYGCRSLIDGIKR 205
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
193 VVNDWKGVSEETTTGVHRLYQIAATGRLLVPAINVDSVTKSKFDNLYGCRSLADGLKR 252
QY |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
206 ATDVMIAGKVAVVAGYGVGCAQALRGFGARVITEIDIPINALQAAMEGYEVTMTDEA 265
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
253 AMDVMIAGKLVAVCGYGVGSAHSLRAYGARVITEIDIPICALQAAMEGFVETVDET 312
QY |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
266 CQSGNIFVTTCIDILGHRHFMKDDAIVCNIGHFDVEIDVKWLNENA-VEKVNIKPQ 324
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
313 LGQADIIVTTTGNKDVIRIEHMTAMKDQVIVCNIGHFDNEIQVDALNALAGVQKINIKPQ 372
QY |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
325 VDRYRLKNGRIILLAEGRVLNLCGANGHPSFVMSNSFTNQVMAQIELWTHDPKYPVGWH 384
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
373 VDKFILPENGNTLLAEGRVLNLCGANGHPSFVMSNSFANQTIAQIDLMQNKDVYEKNVY 432
QY |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
385 FLPKLDEAAVAEHLGKLVNKLTKLTKQAQYLGMSCDGPGPKPDHYRY 432
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
433 RLPKLDDEEVARLHLEKIGVKLTTLTANQAAYLGISVEGPFKEHTRY 480
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Search completed: December 30, 2003, 10:41:05

Job time : 18 secs

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Matches 431; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSKLPYKADIGLAAGWKALDIAENEMPGLMRMRYSASKPLKGARIACGLHMTVET 60
DB 1 MSKLPYKADIGLAAGWKALDIAENEMPGLMRMRYSASKPLKGARIACGLHMTVET 60
QY 61 AVLIETLVLTGAEVQWSSCNIFSTQNHAAATAKAGIPVYAWKGETDEBYLWCIEQTLYF 120
DB 61 AVLIETLVLTGAEVQWSSCNIFSTQDHAAATAKAGIPVYAWKGETDEBYLWCIEQTLYF 120
QY 121 KDGPLNMLDDGGDLTNLIHTKYPQLPGIRGISETTTGVNLYKMMANGILKVPAINV 180
DB 121 KDGPLNMLDDGGDLTNLIHTKYPQLPGIRGISETTTGVNLYKMMANGILKVPAINV 180
QY 181 NDSVTKSFDNLYGCRESLIDGIKRATDVMIAGKVAVAGYDVGKGAQALRGFGARVI 240
DB 181 NDSVTKSFDNLYGCRESLIDGIKRATDVMIAGKVAVAGYDVGKGAQALRGFGARVI 240
QY 241 ITEIDPINALQAAMEGYEVTMTDEACQEGNIFVTTTGCIDIIILGRHFEQMKDDAIVCNIG 300
DB 241 ITEIDPINALQAAMEGYEVTMTDEACQEGNIFVTTTGCIDIIILGRHFEQMKDDAIVCNIG 300
QY 301 HFDVEIDVKWLNENAVEKVNIPQVDYRLKNGRRIILAEGRNLVNLGCMGHPSPVMSN 360
DB 301 HFDVEIDVKWLNENAVEKVNIPQVDYRLKNGRRIILAEGRNLVNLGCMGHPSPVMSN 360
QY 361 SFTNQVMAQIELWTHDPKYPGVGHFLPKLDEAVAEHLGKLVNKLTKLTEKQAQYLGMS 420
DB 361 SFTNQVMAQIELWTHDPKYPGVGHFLPKLDEAVAEHLGKLVNKLTKLTEKQAQYLGMS 420
QY 421 CDGPFKPDHRY 432
DB 421 CDGPFKPDHRY 432

RESULT 2
A26583
adenosylhomocysteinase (EC 3.3.1.1) - rat
N:Alternate names: S-adenosyl-L-homocysteine hydrolase
C:Species: Rattus norvegicus (Norway rat)
C>Date: 19-Nov-1988 #sequence revision 04-Oct-1996 #text_change 18-Jun-1999
C:Accession: A26583; B26191; B26191; S69333
R:Ogawa, H.; Gomi, T.; Mueckler, M.M.; Fujioaka, M.; Backlund Jr., P.S.; Aksamit, R.R.; U
Proc. Natl. Acad. Sci. U.S.A. 84, 719-723, 1987
A:Title: Amino acid sequence of S-adenosyl-L-homocysteine hydrolase from rat liver as de
A:Reference number: A26583; MUID:87118240; PMID:3027698
A:Accession: A26583
A:Molecule type: mRNA
A:Residues: 1-432 <OGA>
A:Cross-references: GB:M15185; NID:G202803; PIDN:AAA40705.1; PID:G202804
R:Gomi, T.; Ogawa, H.; Fujioaka, M.
J. Biol. Chem. 261, 13422-13425, 1986
A:Title: S-Adenosylhomocysteinase from rat liver. Amino acid sequences of the peptides c
A:Reference number: A92560; MUID:87008564; PMID:3759971
A:Accession: A26191
A:Molecule type: protein
A:Residues: 76-94 <GOM>
A:Accession: B26191
A:Molecule type: protein
A:Residues: 104-121 <GO2>
A>Note: in a manner saturably inhibited by adenosine (a product) or adenine (a competi
-79 and Cys-113, suggesting a role for these residues at the active site; however, neith
R:Merta, A.; Aksamit, R.R.; Kasit, J.; Cantoni, G.L.
Eur. J. Biochem. 229, 575-582, 1995
A:Title: The gene and pseudogenes of rat S-adenosyl-L-homocysteine hydrolase.
A:Reference number: S69333; MUID:95262723; PMID:7744082
A:Accession: S69333
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-432 <MER>
A:Cross-references: EMBL:U14937; NID:G1223843; PIDN:AAA32043.1; PID:G1185363
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1994
C:Genetics:

```

A:introns: 10/1; 73/3; 99/1; 149/1; 186/3; 256/1; 285/2; 324/3; 389/3

C:Function: catalyzes the reversible hydrolysis of S-adenosyl-L-homocysteine to adenosylhomocysteinase
C:Superfamily: adenosylhomocysteinase
C:Keywords: homotetramer; NAD; thioether hydrolase
F:214-243/Region: beta-alpha-beta NAD nucleotide-binding fold
F:79,113/Active site: Cys #status predicted

Query Match 96.4%; Score 2189; DB 1; Length 432;

Best Local Similarity 96.3%; Pred. No. 1.2e-153;
Matches 416; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

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QY 1 MSKLPYKADIGLAAGWKALDIAENEMPGLMRMRYSASKPLKGARIACGLHMTVET 60
DB 1 MSKLPYKADIGLAAGWKALDIAENEMPGLMRMRYSASKPLKGARIACGLHMTVET 60
QY 61 AVLIETLVLTGAEVQWSSCNIFSTQNHAAATAKAGIPVYAWKGETDEBYLWCIEQTLYF 120
DB 61 AVLIETLVLTGAEVQWSSCNIFSTQDHAAATAKAGIPVYAWKGETDEBYLWCIEQTLYF 120
QY 121 KDGPLNMLDDGGDLTNLIHTKYPQLPGIRGISETTTGVNLYKMMANGILKVPAINV 180
DB 121 KDGPLNMLDDGGDLTNLIHTKYPQLPGIRGISETTTGVNLYKMMANGILKVPAINV 180
QY 181 NDSVTKSFDNLYGCRESLIDGIKRATDVMIAGKVAVAGYDVGKGAQALRGFGARVI 240
DB 181 NDSVTKSFDNLYGCRESLIDGIKRATDVMIAGKVAVAGYDVGKGAQALRGFGARVI 240
QY 241 ITEIDPINALQAAMEGYEVTMTDEACQEGNIFVTTTGCIDIIILGRHFEQMKDDAIVCNIG 300
DB 241 ITEIDPINALQAAMEGYEVTMTDEACQEGNIFVTTTGCIDIIILGRHFEQMKDDAIVCNIG 300
QY 301 HFDVEIDVKWLNENAVEKVNIPQVDYRLKNGRRIILAEGRNLVNLGCMGHPSPVMSN 360
DB 301 HFDVEIDVKWLNENAVEKVNIPQVDYRLKNGRRIILAEGRNLVNLGCMGHPSPVMSN 360
QY 361 SFTNQVMAQIELWTHDPKYPGVGHFLPKLDEAVAEHLGKLVNKLTKLTEKQAQYLGMS 420
DB 361 SFTNQVMAQIELWTHDPKYPGVGHFLPKLDEAVAEHLGKLVNKLTKLTEKQAQYLGMS 420
QY 421 CDGPFKPDHRY 432
DB 421 INGPFKPDHRY 432

```

RESULT 3

```

JC2480
adenosylhomocysteinase (EC 3.3.1.1) - African clawed frog
N:Alternate names: S-adenosyl-L-homocysteine hydrolase
C:Species: Xenopus laevis (African clawed frog)
C>Date: 29-Mar-1995 #sequence_revision 04-Oct-1996 #text_change 28-May-1999
C:Accession: JC2480
R:Seery, L.T.; McCabe, B.D.; Schoenberg, D.R.; Whitehead, A.S.
Biochem. Biophys. Res. Commun. 205, 1539-1546, 1994
A:Title: S-Adenosyl-L-homocysteine hydrolase from Xenopus laevis: identification, developm
A:Reference number: JC2480; MUID:95110290; PMID:7811234
A:Accession: JC2480
A:Molecule type: mRNA
A:Residues: 1-433 <SEE>
A:Cross-references: GB:L35559; NID:G558507; PIDN:AAA65963.1; PID:G558508
A:Experimental source: liver
C:Function:
adenosylhomocysteinase (EC 3.3.1.1) - African clawed frog
C:Superfamily: adenosylhomocysteinase
C:Keywords: NAD; thioether hydrolase
F:215-244/Region: beta-alpha-beta NAD nucleotide-binding fold
F:79,113/Active site: Cys #status predicted

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Query Match 88.8%; Score 2017.5; DB 1; Length 433;

Best Local Similarity 87.8%; Pred. No. 5.1e-141;
Matches 380; Conservative 28; Mismatches 24; Indels 1; Gaps 1;

QY 1 MSKLPYKADIGLAAGWKALDIAENEMPGLMRMRYSASKPLKGARIACGLHMTVET 60

5 KPAYKADIKLADGPKRKEIIIAENEMPGLMAMRSKYGPSQPLKGARIACGLHMTTQTAVL 64
 64 IETLVTLAGAEVQWSSCNIFSTQNHAAAAIAKAGIPVYAMKGETDEBYLWCIEQTLYPKDG 123
 65 IETLTALGAEVQWSSCNIFSTQDHAAAAIAQTGVPVYAMKGETDEBYEWCIETQIVPKDG 124
 124 -PLNMILDDGGDLTNLHTKYPQLLPGLRIGISETTTGVHNLKWMANGILKVPAINVND 182
 125 QPLNMILDDGGDLTNLHVAKYPOYLAGIRGLSEBTTTGVHNLAKMLAKGDLKVPAINVND 184
 183 SVTSKFDNLYGCRSLIDGIKRATDVMIAAGVAVVAGVDVGKGCACQAALRGFGARVIIT 242
 185 SVTSKFDNLYGIRSLPDGIKRATDVMIAAGVAVVAGVDVGKGSAAASLKAFGSRVIIT 244
 243 EIDPINALQAAAMEGYEVTTMDEACQEGNIFVTTCGICDILGRHPFQMDDAIVCNIGHIF 302
 245 EIDPINALQAAAMEGYEVTTLLEAAPKANIIVTTTGCKDIVTGKHFLLPNDIAIVCNVGHF 304
 303 DVEIDVKWLNENAVEKNIKPQVDVRYRLKNGRIILLLAEGRLVNLGCAMGHSPFVMSNSF 362
 305 DCEIDVKWLNATNATKDTIRKQVDVRYRLKNGRHVILLAEGRLVNLGCATGHPSPFVMSNSF 364
 363 TNQVMAQIELWTH---PDKYPVGVHPPLPKLDEAVAEAHGLKLVNKLTKLTKQAQOYLGM 419
 365 TNQVLAQVELMTKFTQPEYKGLGLVLPKTLDBEAVYLLHLAGVGLTKLSDSQASYLGV 424
 420 SCDPGPKFDHYRY 432
 425 PVAGPYKPDHYRY 437
 RESULT 5
 T40763
 adenosylhomocysteinase - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
 C:Accession: T40763
 R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterh
 submitted to the EMBL Data Library, March 1998
 A:Reference number: Z21948
 A:Accession: T40763
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-433 <LYN>
 A:Cross-references: EMBL:AL022072; PIDN:CAAL7833.1; GSPDB:GN00067; SPDB:SPB8CD
 A:Experimental source: strain 972h-; cosmid c8D2
 C:Genetics:
 A:Gene: SPDB:SPB8CD2.18c
 A:Map position: 2
 C:Superfamily: adenosylhomocysteinase
 Query Match 76.3%; Score 1733; DB 2; Length 433;
 Best Local Similarity 77.1%; Pred. No. 4.8e-120;
 Matches 330; Conservative 40; Mismatches 56; Indels 2; Gaps 2
 7 YKVADIGLAAGRKALDIAENEMPGLMRMRYRSASKPLKGARIACGLHMTVETAVLIET 66
 6 YKVADISLAATGKRKEIIIAENEMPGLIAVREKYAKSQPLKGARIACGLHMTTQTAVLIET 65
 67 LVTLAGAEVQWSSCNIFSTQNHAAAAIAKAGIPVYAMKGETDEBYLWCIEQTL-YFKDG-P 124
 66 LVALGAEVTVWSSCNISTQDHAAAAIAATGVPVPAWKGETEBSYLCIEQQLKSPSPSGPK 125
 125 LNMILDDGGDLTNLHTKYPQLLPGLRIGISETTTGVHNLKWMANGILKVPAINVNDV 184
 126 LNMILDDGGDLTALVHERHPELLVDIRGISETTTGVHNLKPKENKUKLVPAINVNDV 185
 185 TKSFKFDNLYGCRSLIDGIKRATDVMIAAGVAVVAGVDVGKGCACQAALRGFGARVIITI 244
 186 TKSFKFDNLYGCRSLVDGIRKATDVMIAAGVAVVAGVDVGKGCSTSLRSQGARVITVEV 245
 245 DFINALQAAAMEGYEVTTMDEACQEGNIFVTTCGICDILGRHPFQMDDAIVCNIGHFDV 304

Db 246 DPINALQAAMGDFEVTTMBEAEVKGQIFVTTTTCGRDIIRGEHFNEMKEDSIVCNIGHFDV 305
 QY 305 EIDVKWLNENAVEKNIKPQVDYRLKNGRRRIILLAEGRVLNLGCAHGHPSPVMSNSFTN 364
 Db 306 EIDVAVLKANAKADVNNIKPQVDYRLKNGRRRIILLAEGRVLNLGCAHGHPSPVMSNSFTN 365
 QY 365 QVMAQIELWTHPDKYPVGVHFLPKKLDDEAVAEHLGKLVNKLTKLTKTEQAQYLGMSCDGP 424
 Db 366 QVLAQIALWTDNTSYPLGVHMLPKKLDDEAVARHLGKLVNKLTKLTKLTSVQSDYLGIPVDGP 425
 QY 425 FKPDHYRY 432
 Db 426 YKADHYRY 433

RESULT 6

A27655
 N:Adenosylhomocysteinase (EC 3.3.1.1) - slime mold (Dictyostelium discoideum)
 N:Alternate names: S-adenosyl-L-homocysteine hydrolase
 C:Species: Dictyostelium discoideum
 C:Date: 31-Mar-1989 #sequence_revision 04-Oct-1996 #text_change 18-Jun-1999
 C:Accession: A27655; S06394
 R:Kasir, J.; Akemait, R.R.; Backlund Jr., P.S.; Cantoni, G.L.
 Biochem. Biophys. Res. Commun. 153, 359-364, 1988
 A:Title: Amino acid sequence of S-adenosyl-L-homocysteine hydrolase from Dictyostelium d
 A:Reference number: A27655; MUID:88240426; PMID:3288206
 A:Accession: A27655
 A:Molecule type: mRNA
 A:Residues: 1-430 <XAS>
 A:Cross-references: GB:M1937; NID:g167663; PIDN:AAA33165.1; PID:g167664
 R:Guillon, M.C.; Part, D.; Veron, M.
 Biochimie 70, 835-840, 1988
 A:Title: Cloning of a cDNA for the S-adenosyl-L-homocysteine hydrolase from Dictyostelium
 A:Reference number: S06394; MUID:89000991; PMID:3139100
 A:Molecule type: mRNA
 A:Residues: 'VWTKSPKPKPLHYQT', 270-311, 'G', 313-323, 'S', 325-359, 'SVTK', 365-382, 'F', 384-43
 A:Cross-references: EMBL:X12523; NID:g7204; PIDN:CAA31040.1; PID:g7205
 A:Note: this sequence differs at the amino end by an apparent frame shift; comparison to
 C:Function:
 A:Description: catalyzes the reversible hydrolysis of S-adenosyl-L-homocysteine to adeno
 C:Superfamily: adenosylhomocysteinase
 C:Keywords: NAD; thioether hydrolase
 F:213-242/Region: beta-alpha-beta NAD nucleotide-binding fold
 F:78,112/Active site: Cys #status predicted

Query Match 74.7%; Score 1697.5; DB 1; Length 430;
 Best Local Similarity 74.6%; Pred. No. 2e-117;
 Matches 320; Conservative 38; Mismatches 70; Indels 1; Gaps 1;

QY 4 KLPYKVDIGLAAGRKALDIAENEMPGLMRERYASAKPLKGARIAGCLHMTVETAVL 63
 Db 3 KLHYKVDISLAAGRKKEIEIAENEMPGMLTRKKYGPQAIIKLGARIAGCLHMTIQTAVL 62
 QY 64 IETLVTLGAQVWSSCNIFSTQNHAAAAIAKAGIPVYAWKGETDEYLCWICIEQTLYFKDG 123
 Db 63 IETLVTLGAQVWSSCNIFSTQDQAAAAIAAGVPVYAWKGETDEYLCWICIEQTLYFKDG 122
 QY 124 PLNMILDDGGDLTNLIHTKYPQLLPGIRGISETTTGVHNLKYMANGILKVPAINVNDV 183
 Db 123 PLNMILDDGGDLTNLIHTKYPQLLPGIRGISETTTGVHNLKYMANGILKVPAINVNDV 182
 QY 184 VTKSKFDNLGCRSLIDGIKRATDVMIAGKAVVAGYGDVGKCAQALRGFGARVITE 243
 Db 183 VTKSKFDNLGCRSLIDGIKRATDVMIAGKAVVAGYGDVGKCAQALRGFGARVITE 242
 QY 244 IDPINALQAAMEGYEYVTTMDEACQEGNI FVTTTGCIDIIILGRHFEOMKDDAIVCNIGHFD 303
 Db 243 IDPINALQAAMGYQIVTWTETAPLSNIFVTTTGCIDIVRGHFAVWKEDAIVCNIGHFD 302
 QY 304 VEIDVKWLNENAVEKNIKPQVDYRLKNGRRRIILLAEGRVLNLGCAHGHPSPVMSNSFT 363
 Db 303 CBIDVAVLNLANA-KKQTVKPVQVDYRLKNGRRRIILLAEGRVLNLGCGTGHGHPSPVMSNSFC 361

QY 364 NOVMAQIELWTHPDKYPVGVHFLPKKLDDEAVAEHLGKLVNKLTKLTKTEQAQYLGMSCDG 423
 Db 362 NQTLAQIALWTKTEEYPLGVHLLPKLDDEAVARHLDQLGAKLTTLTKTEQSEYLSVPVAG 421
 QY 424 FKPDHYRY 432
 Db 422 PKVDHYRY 430

RESULT 7

S05046
 N:Adenosylhomocysteinase (EC 3.3.1.1) - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YER043c; S-adenosyl-L-homocysteine hydrolase
 C:Species: Saccharomyces cerevisiae
 C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 23-Mar-2001
 C:Accession: S05046
 R:Dieterich, F.S.
 submitted to the EMBL Data Library, December 1994
 A:Description: The sequence of S. cerevisiae cosmid 9379, 9581, and lambda clone 4678.
 A:Reference number: S050432
 A:Accession: S05046
 A:Molecule type: DNA
 A:Residues: 1-449 <DIE>
 A:Cross-references: EMBL:U18796; NID:g603265; PIDN:AAB64578.1; PID:g603276; GSPDB:GN00000
 C:Genetics:
 A:Gene: SGD:SAH1; MIPS:YER043c
 A:Cross-references: SGD:S0000845; MIPS:YER043c
 A:Map position: 5R
 C:Superfamily: adenosylhomocysteinase
 C:Keywords: NAD; thioether hydrolase
 F:214-243/Region: beta-alpha-beta NAD nucleotide-binding fold
 F:80,114/Active site: Cys #status predicted

Query Match 71.9%; Score 1633; DB 2; Length 449;
 Best Local Similarity 70.8%; Pred. No. 1.2e-112;
 Matches 313; Conservative 52; Mismatches 61; Indels 16; Gaps 3;

QY 7 YKVDIGLAAGRKALDIAENEMPGLMRERYASAKPLKGARIAGCLHMTVETAVL 66
 Db 8 YKADIISLAAGRKKEIEIAENEMPGMAIRKAYGVQPLKGARIAGCLHMTIQTAVL 67
 QY 67 LVTLGAQVWSSCNIFSTQNHAAAAIAKAGIPVYAWKGETDEYLCWICIEQTLY-FKDG-P 124
 Db 68 LVALGAQVWSSCNISTQDRAAAAAIAAGVPVYAWKGETDEYLCWICIEQQLFAKDNKK 127
 QY 125 LNMILDDGGDLTNLIHTKYPQLLPGIRGISETTTGVHNLKYMANGILKVPAINVNDV 184
 Db 128 LNLILDDGGDLTNLIHTKYPQLLPGIRGISETTTGVHNLKYMANGILKVPAINVNDV 187
 QY 185 VTKSKFDNLGCRSLIDGIKRATDVMIAGKAVVAGYGDVGKCAQALRGFGARVITE 244
 Db 188 VTKSKFDNLGCRSLIDGIKRATDVMIAGKAVVAGYGDVGKCAQALRGFGARVITE 247
 QY 245 DPINALQAAMEGYEYVTTMDEACQEGNI FVTTTGCIDIIILGRHFEOMKDDAIVCNIGHFDV 304
 Db 248 DPINALQAAMEGYVTTMEDASHIQVFTVTTTGCIDIIINGEHIWNPEDAIVCNIGHFDI 307
 QY 305 EIDVKWLNENAVEKNIKPQVDYRLKNGRRRIILLAEGRVLNLGCAHGHPSPVMSNSFTN 364
 Db 308 EIDVAVLNLANA-KKQTVKPVQVDYRLKNGRRRIILLAEGRVLNLGCGTGHGHPSPVMSNSFC 367
 QY 365 QVMAQIELWTHPDK-----YPGVHFLPKKLDDEAVAEHLGKLVNKLTKL 410
 Db 368 QVLAQIALFKSNDSKSFREKHIEFQKTGPFVGVHVLKILDEAVAKFHLNGLVRLTKLS 427
 QY 411 EKQAOYLGMSCDGPFPKPDHYRY 432
 Db 428 KVQSEYILGIPGEGPKADHYRY 449

RESULT 8

A45569

A;Cross-references: GB:AE003941; GB:AE003849; NID:99105978; PIDN:AAF83847.1; GSPDB:GN001

A;Experimental source: strain 945C

R;Simpson, A.J.G.; Rainach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Algr

B;Rios, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrato, D.M.; Carroer, H

as-Neto, E.; Docena, C.; El-Dorty, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohne

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurame, E.E.; Laigre

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martino, E

A;Authors: Martins, E.M.P.; Matukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Vertovaki-Almeida, S.; Vettore, A.L.; Z

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XP1037

C;Superfamily: adenosylhomocysteinease

Query Match 59.1%; Score 1342; DB 2; Length 446;

Best Local Similarity 61.0%; Pred. No. 3.2e-91;

Matches 272; Conservative 49; Mismatches 83; Indels 42; Gaps 6;

Qy 29 MPGLMRWRVRSYASKPLKGARIAGCLHMTVETAVLIETLVTLGARVQWSSCNIFSTQNH 88

Db 1 MPGLMSIRKVKYASKQPLKGVRTVGSLSHTIQTAVLIETLTKDGVARVWASCNIFSTQDHA 60

Qy 89 AAAATAGAGIPYANKGETDEEYLACIEQTLYP--KDGPL---NMILDDGGDLTLNLHTKY 143

Db 61 AAAATAGSGTPVFAWKGETLEEYWDCTLQALFTLSGDTLTGPELIVDDGGDATLLIHKG 120

Qy 144 -----PQLL-----PGI-----RGISEETTTGTVHNLVKM 167

Db 121 ELENGSTWDEPDSLSERQVTKRLKRTAIEPRGYWTRVNDWKGVSEETTTGVHRLYQI 180

Qy 168 MANGILKVPAINVDSVTKSPDNLYGCRSLIDGKIKRATVMIAGKVAVAVGVDVGKG 227

Db 181 AATGRLLVPAINVDSVTKSPDNLYGCRSLADGLKRAMDVMLAGKLAVCVGVGVDVGKG 240

Qy 228 CAQALRFGARVITETDPIVALQAMGEYVTTWDEACQEGNIFVTTGCCIDILGRHP 287

Db 241 SAHSLRAYGARVITETDPICALQAMGEFVTTVEDTLGQADIVYVTTTGNKQVIRIEHM 300

Qy 288 EQMKDDATVCNIGHFDVEIDVKMLNENA-VEKNVTKPQVDYRLKXGRRILLAEGRLVN 346

Db 301 TAMKQDVIVCNIGHFDNEIQVDALNALAGVQKINIKPQVDKFLPNGNTFLAEGRLVN 360

Qy 347 LGCAMGHPSFVMSNSFTNQVMAQIELWTHPDKPYGVGHFLPKKLDEAVABAHGLKLVKL 406

Db 361 LGCATGHPSFVMSNSFANOTLAQIDLWKNQVYKXNVYRLPKKLDEEVARLHLEKIGVKL 420

Qy 407 TKLTEQAQYLGMSCDGPFKPDHYRY 432

Db 421 TTLTANQAAYLGISVEGPFKPEHYRY 446

RESULT 10

S38379

adenosylhomocysteinease (EC 3.3.1.1) - Madagascarcari periwinkle

N;Alternate names: S-adenosyl-L-homocysteine hydrolase

C;Species: Catharanthus roseus (Madagascarcari periwinkle)

C;Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S38379

R;Schroeder, G.; Waitz, A.; Hotze, M.; Schroeder, J.

submitted to the EMBL Data Library, October 1993

A;Description: cDNA for stress-induced S-adenosyl-L-homocysteine hydrolase from Madagascarcari

A;Reference number: S38379

A;Accession: S38379

A;Molecule type: DNA

A;Residues: 1-485 <SCH>

A;Cross-references: EMBL:Z26881; NID:g407411; PIDN:CAA81527.1; PID:g407412

C;Genetics:

Db 58 AVLIETLKALGADVRWASCNIFSTQDHAIAAIAAGTVPFAVKGETLBEYWAYTKIFQF 117
 QY 121 KQGLPMILDDGGDL-----TNLIHTK-----Yp 144
 Db 118 PEGTCNMILDDGGDATLYILLGARVEAGETDLIATTSDEVCFLPQIKRWVESPGWT 177
 QY 145 QLLPGIRGISEETTTGVHNLKYMANGILKVPAINVDSVTKSPFNLYGCRSLIDGK 204
 Db 178 QQRAAIKGVSEETTTGVHRLYDLKKGGLLPFAINVDSVTKSPFNLYGCRSLVDGIR 237
 QY 205 RATDVMIAKAVVAGYGVGKCAQALRGFGARVLIITEIDPINALQAAAMEGVETVMD 264
 Db 238 RATDVMIAKAVVAGYGVGKCAQALRGFGARVLIITEIDPINALQAAAMEGVETVMD 297
 QY 265 ACQEGNIFVTTCIDIIILGRHFEQMKDDAIVCNIGHFDVEIDV-----KMLNENAVEK 318
 Db 298 VVADA-IFITTTGNKDVIRIEHWRMKDMAIVGNIGHFDNEIOVAALKKHK----- 348
 QY 319 VNIKPOVDYRLKNGRRILLAEGRVLNLCGAMGHPSPFVMSNFTNQVMAQIELWTHPK 378
 Db 349 TNIKQDQMIEMPSGARIILSLSEGRLLNLTGNATGHPSPFVMSNFTNQVMAQIELWTHPK 408
 QY 379 YPVGVHFLPKLDEAVAEHLGKLVNLTKEQAQYLGMSCDGPFKPDHYRY 432
 Db 409 YOPGVYILPKSLDEKVARLHLKIGVKTTLRDPQAEYIGVTVEGPFKSDHYRY 462
 RESULT 13
 D87005
 probable S-adenosyl-L-homocysteine hydrolase [imported] - Mycobacterium leprae
 C:Species: Mycobacterium leprae
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
 C:Accession: D87005
 R: Cole, S.T.; Eiglsmeier, K.; Parthill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
 R.; Davies, R.M.; Devlin, K.; Duthey, S.; Feltwell, T.; Frazer, A.; Hamlin, N.; Holroyd,
 eam, M.A.; Rutherford, K.M.
 Nature 409, 1007-1011, 2001
 A:Title: Massive gene decay in the leprosy bacillus.
 A:Reference number: A86909; MUID:21128732; PMID:11234002
 A:Accession: D87005
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-492 <STO>
 A:Cross-references: GB:AL450380; NID:gl3092881; PIDN:CAC30280.1; GSPDB:GN00147
 A:Gene: sahH
 C:Superfamily: adenosylhomocysteinease
 Query Match 57.4%; Score 1302.5; DB 2; Length 492;
 Best Local Similarity 55.6%; Pred. No. 3e-88;
 Matches 265; Conservative 58; Mismatches 105; Indels 49; Gaps 4;
 QY 5 LPYKVADIGLAAGWKALDIAENMPGLMRERYASAKPLKGARIAGCLHMTVETAVLI 64
 Db 16 IDPKVADLSANFGKELDLAEYMPGLMSLRHEYAEVQPLKGARISGLHMTVQTA 75
 QY 65 ETLLTALGAEVQWSSCNIFSTQDHAIAAIA-----KAGIPYAWKGETDEBYLW 115
 Db 76 ETLLTALGAEVQWSSCNIFSTQDHAIAAIAVVGYPGTPPEPKGVFPFAWKGETLE 135
 QY 116 QTLYF--KQGLPMILDDGGDLTNLI----- 139
 Db 136 QMTWFPDPKPVNMLDDGGDATMLVLRGVQYKAGVVPFAEVDDSAEWKVFNLRLKRP 195
 QY 140 ---HTKYPQLLPGIRGISEETTTGVHNLKYMANGILKVPAINVDSVTKSPFNLYGCR 196
 Db 196 ETDGKWTAKIASKVGVTEBTTTGVRLYQFAAAGDLAPPAINVDSVTKSPFNLYGCR 255
 QY 197 ESLIDGIRKATDVMIAKAVVAGYGVGKCAQALRGFGARVLIITEIDPINALQAAAMEG 256
 Db 256 HSLIDGIRKATDVMIAKAVVAGYGVGKCAQALRGFGARVLIITEIDPINALQAAAMEG 315

QY 257 YEVTMTDEACQEGNIFVTTCIDIIILGRHFEQMKDDAIVCNIGHFDVEIDVKNL 316
 Db 316 PDVKRVEDVIADSDIVVTATGNKDIILHEHMKAMKHAILGNIGHFDNEIMAA 375
 QY 317 EKVNKIPQVDYRLKNGRRILLAEGRVLNLCGAMGHPSPFVMSNFTNQVMAQIELWTH 375
 Db 376 TRLNLTNIPQVDLWTFGSGKSIIVLSEGRLLNLTGNATGHPSPFVMSNFTNQVMAQIELWTH 435
 QY 376 PDYKYPGVHFLPKLDEAVAEHLGKLVNLTKEQAQYLGMSCDGPFKPDHYRY 432
 Db 436 NDDYDNEVYRLPKHLDEKVARVHVAALGGQLTKLTKDQAEYLGVDVDPKPDHYRY 492
 RESULT 14
 AG3505
 adenosylhomocysteinease (EC 3.3.1.1) [imported] - Brucella melitensis (strain 16M)
 C:Species: Brucella melitensis
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
 C:Accession: AG3505
 R: DelVecchio, V.G.; Kaprat, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova, T.;
 Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesec
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AG3505
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-481 <KUR>
 A:Cross-references: GB:AE008917; PIDN:AAL53210.1; PID:gl7984086; GSPDB:GN00190
 A:Experimental source: strain 16M
 C:Genetics:
 A:Map position: 1
 C:Superfamily: adenosylhomocysteinease
 C:Keywords: thioether hydrolase
 Query Match 57.3%; Score 1302; DB 2; Length 481;
 Best Local Similarity 57.2%; Pred. No. 3.2e-88;
 Matches 271; Conservative 52; Mismatches 101; Indels 50; Gaps 6;
 QY 1 MSDKLPYKVADIGLAAGWKALDIAENMPGLMRERYASAKPLKGARIAGCLHMTVET 60
 Db 16 MTASQDFVVKQISLADWGRRELDIAETEMPGMLAAREEFKSGPLKGARISGLHMTIQT 75
 QY 61 AVLIETLTLGAEVQWSSCNIFSTQDHAIAAIAKAGIPYAWKGETDEBYLWCIETLYF 120
 Db 76 AVLIETLTLGAEVQWSSCNIFSTQDHAIAAIAATGTPVFAVKGETLEBYTYTDDI 135
 QY 121 KDG-PLNMLDDGGDLTNLI-----HTKYPQL-----LPG--- 149
 Db 136 PDGEPNMLDDGGDATMYILLGARAEAGEDVLSNPQSEEBEVLPAQIKRMAATPGPT 195
 QY 150 -----IRGISEETTTGVHNLKYMANGILKVPAINVDSVTKSPFNLYGCRSLIDGK 204
 Db 196 KQRAAIKGVTEBTTTGVHNLKYMANGILKVPAINVDSVTKSPFNLYGCRSLIDGK 255
 QY 205 RATDVMIAKAVVAGYGVGKCAQALRGFGARVLIITEIDPINALQAAAMEGVETVMD 264
 Db 256 RGTDMVMAKAVVAGYGVGKCAQALRGFGARVLIITEIDPINALQAAAMEGVETVMD 315
 QY 265 ACQEGNIFVTTCIDIIILGRHFEQMKDDAIVCNIGHFDVEIDV-----KMLNENAVEK 318
 Db 316 AASTADIVTTTGNKDVIRIEHWRMKDMAIVGNIGHFDNEIOVAALKKHK----- 367
 QY 319 VNIKPOVDYRLKNGRRILLAEGRVLNLCGAMGHPSPFVMSNFTNQVMAQIELWTHPK 378
 Db 368 TNVKEQVLDIEPDPGKRLILLSEGRLLNLTGNATGHPSPFVMSNFTNQVMAQIELWTHPK 427
 QY 379 YPVGVHFLPKLDEAVAEHLGKLVNLTKEQAQYLGMSCDGPFKPDHYRY 432
 Db 428 YKNEVYVLPKHLDEKVARLHLKIGVKTTLVSEQAQYIGVTVEGPFKSDHYRY 481

RESULT 15

AF2580
S-adenosylhomocysteine hydrolase ahcy [imported] - Agrobacterium tumefaciens (strain C58)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AF2580
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:21608550; PMID:11743193
A:Accession: AF2580
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-466 <KUR>
A:Cross-references: GB:AE008688; PIDN:AAL41060.1; PID:g17738347; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: ahcy
A:Map position: circular chromosome
C:Superfamily: adenosylhomocysteinase

	Query Match	57.2%	Score 1299;	DB 2;	Length 466;
	Best Local Similarity	57.6%;	Pred. No. 5.1e-88;		
	Matches 273;	Conservative 51;	Mismatches 100;	Indels 50;	Gaps 5;
QY	1	MSDKLPYKVDIGLAAMGRKALDIAENEMPGLMRMEERYASKPLKRGARIAGCLHMTVET	60		
DB	1	MSLEKDYIVADINLAAGFKELDIAETEMFGLMSCKRFGESKPLKAGARITGSLHMTIQT	60		
QY	61	AVLIETLVILGARVQWSSCNIFSTQNHAAAAIAKAGIPYAWKGETDEYLMCIEQTLYP	120		
DB	61	GVLIETLKEIGAIRWASCNIFSTQDHAAAAIAAGIPVFAVKGESLTYEYETDKIFQW	120		
QY	121	KDGPL-NMILDDGGDLTNLI-----HTKYPQLLPG----	149		
DB	121	TGGLSNMILDDGGDAITWYLLGARAEAGEDVLSNPGSEBEILPAQINKRLKASPGWFT	180		
QY	150	-----IRGISEETTGVHNLKMMANGILKVPAINVNDSVTKSKPDNLYGCRESLIDGIK	204		
DB	181	KQDALKGVTETTTGVHRLYDLAKKGLLPFPAINVNDSVTKSKPDNLYGCRESLVDGIR	240		
QY	205	RATDVMIAKVAVAGYGVGKCAQALRGFGARVITTEIDPINALQAAWEGYEYTTMDE	264		
DB	241	RATDVMAGKVAVCGYGVGKSAASLQAGARVKVTEIDPICALQAAWDGFEVVRLED	300		
QY	265	ACQEGNIFVTTCIDPILGRHFEQMKDDAIVCNIGHDPVEIDV-----KMLNENAVEK	318		
DB	301	VYSSADIFITTTGNKDVIRIEHREMKDMAIVGNIGHDPNEIQVASLRNLKW-----	352		
QY	319	VNIKQVDRYRLKNGRRIILLAEGRVLNLCGAMGHPFVMSNFTNQVMAQIELWTHDPK	378		
DB	353	TNIKQVDMIEPPKGNRIILLSEGRLLNLGNATGHPFVMSASFTNQVLGQIELFTKPGC	412		
QY	379	YPVGWHLFPKLDVAEVAEHLKLVKLTQKQAYLGMSCDGPFKPDHYRY	432		
DB	413	YKNEVYLPKHLDEKVARLHLEKLVRLTELSLDQADYIGISKQGPFAEHYRY	466		

Search completed: December 30, 2003, 10:42:32
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:36:48 ; Search time 46 Seconds
(without alignments)
1490.650 Million cell updates/sec

Title: US-10-043-787-1

Perfect score: 2271

Sequence: 1 MSDKLPYKVDIGLAAGRK.....QAQYLGMSCDGPFKPDHYRY 432

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_19Jun03.*

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1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
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19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2266	99.8	457	21	AA43614
2	2204.5	97.1	433	23	AA25380
3	1819.5	80.1	432	22	AB70895
4	1393	61.3	469	24	ABU11410
5	1315.5	57.9	495	21	AAV87873
6	1297	57.1	485	21	AA34060
7	1297	57.1	510	21	AA34059
8	1296	57.1	486	13	AA26500
9	1292	56.9	485	21	AA40086

10	1292	56.9	508	21	AA40085
11	1289	56.8	485	17	AAW01458
12	1274	56.1	485	21	AA41407
13	1274	56.1	497	21	AA41406
14	1272	56.0	467	21	AA40087
15	1254	55.2	467	21	AA41408
16	1248	55.0	450	21	AA34061
17	1242	54.7	478	22	AAU71911
18	1242	54.7	478	22	AAU71911
19	1242	54.7	498	22	AAU7842
20	1238	54.5	474	22	AAU7842
21	1236	54.4	485	17	AAW01459
22	1224	53.9	467	21	AA22957
23	1224	53.9	489	21	AA22956
24	1204	53.0	449	21	AA22958
25	1151	50.7	614	19	AAW56097
26	1149.5	50.6	504	22	AB71710
27	1149.5	50.6	521	22	AB58663
28	1146	50.5	500	20	AAW90061
29	1139	50.2	564	23	ABG3271
30	1098	48.3	432	22	AAU71913
31	1098	48.3	432	22	AAU71913
32	1084	47.7	395	23	AAE25390
33	878.5	38.7	422	22	AAW98504
34	870	38.3	170	23	AAW9455
35	779	34.3	455	22	ABG12029
36	761	33.5	464	21	AAU77950
37	423	18.6	500	23	ABP65910
38	416.5	18.3	410	22	ABG27861
39	415	18.3	81	21	AAW01918
40	415	18.3	97	16	AAW80298
41	394	17.3	95	16	AAW80297
42	385	17.0	135	22	AAO10323
43	296	13.0	66	23	ABP42348
44	291	12.8	89	23	ABP42055
45	276.5	12.2	312	22	ABG12030

ALIGNMENTS

RESULT 1

AA43614

ID AAB43614 standard; Protein; 457 AA.

XX AAB43614;

XX 08-FEB-2001 (first entry)

XX Human cancer associated protein sequence SEQ ID NO:1059.

Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cyclostatic; proliferative; vulnerable; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antithrombotic; antitumor; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antiproliferative; angiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.

OS Homo sapiens.

XX WO20005350-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US05882.

XX 12-MAR-1999; 99US-0124270.

XX (HUMA-) HUMAN GENOME SCI INC.

PA

XX Rosen CA, Ruben SM;
PI WPI; 2000-587533/55.
DR N-PSDB; AAC77823.
XX Novel isolated nucleic acids comprising sequences encoding peptides
PT useful for treating or diagnosing e.g. cancer -
XX Claim 11; Page 1650-1652; 2352pp; English.
XX AAC77607 to AAC78448 encode the human cancer associated proteins given
CC in ABA43398 to ABA44239. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; vulnary; immunomodulator;
CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
CC antiinflammatory; antithyroid; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC neotropic; vasotropic; antipsoriatic and antiangiogenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC Polynucleotides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating
CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autoimmune
CC disorders, allergic reactions, graft versus host disease, and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies,
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and ABA44240 represent sequences used in the exemplification of
CC the present invention.
XX Sequence 457 AA;
SQ

Query Match 99.8%; Score 2266; DB 21; Length 457;
Best Local Similarity 99.8%; Pred. No. 5e-226;
Matches 431; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKLPYKVDIGLAAGRWKALDIAENEMPLMRERYASXPLKAGIAGLHMTVET 60
DB 26 MSKLPYKVDIGLAAGRWKALDIAENEMPLMRERYASXPLKAGIAGLHMTVET 85
QY 61 AVLIETLVLAGAEVQWSSCNIFSTONHAAAIAKAGIPVYAWKGETDEEVLWCIEQTLF 120
DB 86 AVLIETLVLAGAEVQWSSCNIFSTQDHAIAIAKAGIPVYAWKGETDEEVLWCIEQTLF 145
QY 121 KDGPLNMILDDGDLNLNLTHTKYPQLLPGLRGISEETTTGVHNLKXWANGILKVPAINV 180
DB 146 KDGPLNMILDDGDLNLNLTHTKYPQLLPGLRGISEETTTGVHNLKXWANGILKVPAINV 205
QY 181 NDSVTKSKFDNLVGCRESLIDGIKRATDVMIAGKAVVAGYGVGKGCQALRGFGARVI 240
DB 206 NDSVTKSKFDNLVGCRESLIDGIKRATDVMIAGKAVVAGYGVGKGCQALRGFGARVI 265
QY 241 ITEIDPINALQAAMEGVETVTDACQEGNIFVTTTGCTDIIILGRHFQMKDAIVCNIG 300
DB 266 ITEIDPINALQAAMEGVETVTDACQEGNIFVTTTGCTDIIILGRHFQMKDAIVCNIG 325
QY 301 HFDVEIDVKWLNENAVEKVNIPQVDYRLKNGRRILLAEGRVLNLCAMGHPSPVMSN 360
DB 326 HFDVEIDVKWLNENAVEKVNIPQVDYRLKNGRRILLAEGRVLNLCAMGHPSPVMSN 385
QY 361 SFTNQWMAQIELTHDPKVPVGVHFLPKLDEAVAHAHGLKLVKLTKEQAQYLGM 420
DB 386 SFTNQWMAQIELTHDPKVPVGVHFLPKLDEAVAHAHGLKLVKLTKEQAQYLGM 445
QY 421 CDGPFKPDHYRY 432
DB 446 CDGPFKPDHYRY 457

RESULT 2

AAE25380
ID AAE25380 standard; Protein; 433 AA.
XX
AC AAE25380;
XX
DT 30-OCT-2002 (first entry).
XX
DE Human NZMS-4 protein.
XX
XX Human; enzyme; NZMS-4; cell proliferative disorder; hepatitis; cancer;
KW psoriasis; leukaemia; autoimmune disorder; diabetes; arteriosclerosis;
KW acquired immune deficiency syndrome; cardiovascular disorder; anorexia;
KW asthma; hypertension; gastrointestinal disorder; reproductive disorder;
KW gastritis; neurological disorder; epilepsy; pulmonary disorder; AIDS;
KW dementia; embolism; gene therapy; eye disorder; transgenic.
XX
OS Homo sapiens.
XX
PN WO200246385-A2.
XX
PD 13-JUN-2002.
XX
PF 04-DEC-2001; 2001WO-US47432.
XX
XX 07-DEC-2000; 2000US-251824P.
PR 08-DEC-2000; 2000US-254312P.
PR 14-DEC-2000; 2000US-255773P.
PR 15-DEC-2000; 2000US-255940P.
PR 15-DEC-2000; 2000US-256188P.
PR 21-DEC-2000; 2000US-257488P.
PR 19-JAN-2001; 2001US-262839P.
PR 26-JAN-2001; 2001US-264402P.
XX
XX (INCY-) INCYTE GENOMICS INC.
PA
XX
XX Tang YT, Griffin JA, Yue H, Lee EA, Baughn MR, Duggan BM;
PI Walla NK, Lee S, Ramkumar J, Warren BA, Gandhi AR, Lu DM, Lu Y;
PI Yao MG, Ding L, Tribouley CM, Sanjanwala MM, Arvizu C, Hillman JL;
XX
XX WPI; 2002-537565/57.
DR N-PSDB; AAD411391.
XX
PT Novel human enzyme, NZMS useful in diagnosis, prevention or treatment
PT of cell proliferative, autoimmune/inflammatory, cardiovascular,
PT gastrointestinal, neurological, pulmonary, reproductive and eye
PT disorders -
XX
PS Claim 59; Page 139-140; 173pp; English.
XX
XX The invention relates to human enzymes designated NZMS and nucleic
CC acid molecules encoding such proteins. Sequences of the invention
CC are useful for diagnosing, treating or preventing disorders associated
CC with aberrant expression of NZMS. The disorders treated include
CC cell proliferative disorders such as hepatitis, psoriasis, cancer
CC (e.g. leukaemia), autoimmune disorders such as diabetes, acquired
CC immune deficiency syndrome (AIDS), cardiovascular disorders such as
CC arteriosclerosis, hypertension), gastrointestinal disorders (e.g.
CC anorexia, gastritis), neurological disorders (e.g. epilepsy, dementia),
CC pulmonary disorders (e.g. embolism, asthma), reproductive or eye
CC disorders. Polypeptides of the invention is useful in a number of drug
CC screening techniques and to analyse the proteome of a tissue or cell
CC type. They are also useful as elements on a microarray. Polynucleotides
CC of the invention are useful for creating knockin humanised animals or
CC transgenic animals to model human diseases, in somatic or germline gene
CC therapy, to generate a transcript image of a tissue or cell type, for
CC detecting difference in the chromosomal location due to translocation
CC or inversion among normal, carrier or affected individuals and as
CC hybridisation probes for mapping naturally occurring genomic sequences.
CC The present sequence is human NZMS protein.
XX
SQ Sequence 433 AA;
Query Match 97.1%; Score 2204.5; DB 23; Length 433;

Best Local Similarity 97.2%; Pred. No. 1.1e-219; Matches 421; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 1 MSKPKYKADIGLAAGKALDIAENEMPGLMRERYASAKPLKARIAGLHMTVET 60
DB 1 MSKPKYKADIGLAAGKALDIAENEMPGLMRERYASAKPLKARIAGLHMTVET 60
QY 61 AVLIETLVITGAQVQWSSCNIFSTQNHAAIAKAGIPYVAKGETDEEYLWCIEQTLVF 120
DB 61 AVLIETLVITGAQVQWSSCNIFSTQNHAAIAKAGIPYVAKGETDEEYLWCIEQTLVF 120
QY 121 KQPLNMLDDGGDLNLHTKYPQLLPGIRGISEETTTGVHNLKYMANGILKVPAINV 180
DB 121 KQPLNMLDDGGDLNLHTKYPQLLPGIRGISEETTTGVHNLKYMANGILKVPAINV 180
QY 181 NDSVTK-SKFDNLYGCRSLIDGIKRATDVMIAGKAVVAGYDVGKCAQALRGFGARV 239
DB 181 NDSVTK-SKFDNLYGCRSLIDGIKRATDVMIAGKAVVAGYDVGKCAQALRGFGARV 240
QY 240 IITEIDIPINALQAAMEGYEVTMTDEACQEGNIFVTTTGCIDIIILGRHFEQMKDDAIVCNI 299
DB 241 IITEIDIPINALQAAMEGYEVTMTDEACQEGNIFVTTTGCIDIIILGRHFEQMKDDAIVCNI 300
QY 300 GHFDVIDVKWLNENAVEKNIRKQVDYRLKNGRRIILAEGLRNLGCMGHPGFVMS 359
DB 301 GHFDVIDVKWLNENAVEKNIRKQVDYRLKNGRRIILAEGLRNLGCMGHPGFVMS 360
QY 360 NSFTNQMAQIELWTHDPKYPGVHFLPKLDEAVAEHLGKLVNKLTKLTKTEQAQYLG 419
DB 361 NSFTNQMAQIELWTHDPKYPGVHFLPKLDEAVAEHLGKLVNKLTKLTKTEQAQYLG 420
QY 420 SCGPKPDHRY 432
DB 421 PIDGPKPDHRY 433

RESULT 3
ABB70895
ID ABB70895 standard; Protein; 432 AA.
AC ABB70895;
XX
XX
DT 26-MAR-2002 (first entry)
DE Drosophila melanogaster polypeptide SEQ ID NO 39477.
XX Drosophila melanogaster polypeptide; cell signalling; insecticide;
KW pharmaceutical.
XX Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL14998.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Disclosure; SEQ ID NO 39477; 21pp + Sequence Listing; English.
XX

CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 432 AA;

Query Match 80.1%; Score 1819.5; DB 22; Length 432;
Best Local Similarity 80.7%; Pred. No. 1.1e-179; Indels 1; Gaps 1;
Matches 347; Conservative 28; Mismatches 54;

QY 4 KLPYKADIGLAAGKALDIAENEMPGLMRERYASAKPLKARIAGLHMTVETAVL 63
DB 3 KPSYKADISLAEGWKALIIAENEMPGLMACKKYPSPKPLKARITGCLHMTVQTAVL 62
QY 64 IETLVITGAQVQWSSCNIFSTQNHAAIAKAGIPYVAKGETDEEYLWCIEQTLVPDG 123
DB 63 IETLVITGAQVQWSSCNIFSTQNHAAIAKAGIPYVAKGETDEEYLWCIEQTLVPDG 122
QY 124 -PLNMLDDGGDLNLHTKYPQLLPGIRGISEETTTGVHNLKYMANGILKVPAINVND 182
DB 123 QPLNMLDDGGDLNLHTKYPQLLPGIRGISEETTTGVHNLKYMANGILKVPAINVND 182
QY 183 SVTKSKFDNLYGCRSLIDGIKRATDVMIAGKAVVAGYDVGKCAQALRGFGARVIT 242
DB 183 SVTKSKFDNLYGCRSLIDGIKRATDVMIAGKAVVAGYDVGKCAQALRGFGARVIT 242
QY 243 EIDPINALQAAMEGYEVTMTDEACQEGNIFVTTTGCIDIIILGRHFEQMKDDAIVCNI 302
DB 243 EVDIPINALQAAMEGYEVTMTDEACQEGNIFVTTTGCIDIIILGRHFEQMKDDAIVCNI 302
QY 303 DVEIDVKWLNENAVEKNIRKQVDYRLKNGRRIILAEGLRNLGCMGHPGFVMSNSF 362
DB 303 DVEIDVKWLNENAVEKNIRKQVDYRLKNGRRIILAEGLRNLGCMGHPGFVMSNSF 362
QY 363 TNQVMAQIELWTHDPKYPGVHFLPKLDEAVAEHLGKLVNKLTKLTKTEQAQYLGMS 422
DB 363 TNQVMAQIELWTHDPKYPGVHFLPKLDEAVAEHLGKLVNKLTKLTKTEQAQYLG 422
QY 423 GPFKPDHRY 432
DB 423 GPFKPDHRY 432

RESULT 4
ABU11410
ID ABU11410 standard; Protein; 469 AA.
XX
XX AC ABU11410;
XX
XX
DT 11-FEB-2003 (first entry)
DE
DE
XX Protein encoded by S. atroolivaceus leinamycin gene cluster ORF+8.
XX Leinamycin biosynthesis gene cluster; Lmn; open reading frame; ORF;
KW anti-tumour antibiotic; broad spectrum antimicrobial activity;
KW Gram-positive; Gram-negative bacteria; chemical modification;
KW metabolite; apo-carrier protein; holo-carrier protein; tumour;
KW polyketide; hybrid polyketide/polyketide metabolite; Lmn production;
XX cytosolic.
XX
OS Streptomyces atroolivaceus.
XX
PN WO200277179-A2.
XX
XX 03-OCT-2002.

CC sequence represents a Microbacterium tuberculosis TB54 antigen
described in the invention.

XX
SQ Sequence 495 AA;

Query Match 57.9%; Score 1315.5; DB 21; Length 495;
Best Local Similarity 55.8%; Pred. No. 2.9e-127;
Matches 266; Conservative 61; Mismatches 101; Indels 49; Gaps 5;

QY	5	LPYKVDIGLAAGRKALDAENEMGLMRRYRSASKPLKARITAGCLHMTVETAVLI	64
DB	19	IDFKIADLSLADFGREKRLTAHEHMLSLREYAEVQLKARISGSLHMTVQFVAVLI	78
QY	65	ETLVTILGAEQWSSCNIFSTQNHAAAAIA-----KAGIPVYAWKGETDEEYLWCIE	115
DB	79	ETLTALGAERVWASCNIFSTQDHAAAAVVVPHGTPDEPKGVFVFAWKGETLEEYVWAAE	138
QY	116	QTYLP--KUGPLNMLDDGGDLT-----NLHT--	141
DB	139	QMLTWPPDKPANMLDDGGDATMLVLRGMQYKAGVVPPEEDDPAEWKVFLLRLTRF	198
QY	142	-----KYPQLLPGIRGSEETTTGVHLYKWMANGILKVPAINVNDVSKSKEDNLYGCR	196
DB	199	ETDKWTKIAESVKGVTETTTGVRLRYQFAAGDLAPPAINVNDVSKSKEDNLYGTR	258
QY	197	ESLIDGIKRATDVMIAGKAVAVAGYGVGKCAQALRGFGARVITTEIDPINALQAAWEG	256
DB	259	HSLLIDGINRTDALIGKGLVLCYGVGKCAEMKGGQARVSVTEIDPINALQAAWEG	318
QY	257	YEVTWDEACQEGNIFVTTTGCIDIIILGRHFEQKDDAIVCNIGHFDEIDVKMLNENAV	316
DB	319	FVVTVVEEAIGDADIVVTATGNKDIIMLEHIKAKDHAILLGNIGHFDEIDMAGLERSGA	378
QY	317	EKNVIRPOVDRYRL-KNGRRIILLAEGRILNLCAMGHPSPVMSNFTNQVMAQIELWTH	375
DB	379	TRYNVRPQVDLWTFGTGTRSIIIVLSEGRLLNGLNATGHPSPVMSNFPANQIAQIELWTK	438
QY	376	PDKYPGVVHPLPKLDEAAVAZHLKLVNKLTKLTKAQOYLGWSCDGPPEKPDHYRY	432
DB	439	NDEYDNEVYRPLKHLDEKVARIHVEALGGHLTKLTKAQOYLGVDVGGPKPDHYRY	495

RESULT 6

AAG34060

ID AAG34060 standard; Protein; 485 AA.

AC AAG34060;

XX

XX

DT 18-OCT-2000 (first entry)

DE

DE Zea mays protein fragment SEQ ID NO: 41387.

XX

XX

KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; Genetic mapping; gene expression control; promoter;
termination sequence; Corn.

KW

XX

XX

OS Zea mays subsp. mays.

XX

XX

FN EP1033405-A2.

XX

XX

PD 06-SEP-2000.

XX

XX

PF 25-FEB-2000; 2000EP-0301439.

XX

XX

PR 25-FEB-1999; 99US-0121825.

PR

PR 05-MAR-1999; 99US-0123180.

PR

PR 09-MAR-1999; 99US-0123548.

PR

PR 23-MAR-1999; 99US-0125788.

PR

PR 25-MAR-1999; 99US-0126284.

PR

PR 23-MAR-1999; 99US-0126785.

PR

PR 01-APR-1999; 99US-0127462.

PR

PR 06-APR-1999; 99US-0128234.

PR

PR 08-APR-1999; 99US-0128714.

PR

PR	16-APR-1999;	99US-0129845.
PR	19-APR-1999;	99US-0130077.
PR	21-APR-1999;	99US-0130449.
PR	23-APR-1999;	99US-0130510.
PR	23-APR-1999;	99US-0130891.
PR	28-APR-1999;	99US-0131449.
PR	30-APR-1999;	99US-0132048.
PR	04-MAY-1999;	99US-0132407.
PR	05-MAY-1999;	99US-0132484.
PR	06-MAY-1999;	99US-0132485.
PR	06-MAY-1999;	99US-0132486.
PR	06-MAY-1999;	99US-0132487.
PR	07-MAY-1999;	99US-0132863.
PR	11-MAY-1999;	99US-0134256.
PR	14-MAY-1999;	99US-0134218.
PR	14-MAY-1999;	99US-0134219.
PR	14-MAY-1999;	99US-0134221.
PR	14-MAY-1999;	99US-0134370.
PR	18-MAY-1999;	99US-0134768.
PR	19-MAY-1999;	99US-0134941.
PR	20-MAY-1999;	99US-0135124.
PR	21-MAY-1999;	99US-0135153.
PR	24-MAY-1999;	99US-0135629.
PR	25-MAY-1999;	99US-0136021.
PR	27-MAY-1999;	99US-0136392.
PR	28-MAY-1999;	99US-0136782.
PR	01-JUN-1999;	99US-0137222.
PR	03-JUN-1999;	99US-0137528.
PR	04-JUN-1999;	99US-0137502.
PR	07-JUN-1999;	99US-0137724.
PR	08-JUN-1999;	99US-0138094.
PR	10-JUN-1999;	99US-0138054.
PR	10-JUN-1999;	99US-0138847.
PR	14-JUN-1999;	99US-0139119.
PR	16-JUN-1999;	99US-0139452.
PR	16-JUN-1999;	99US-0139453.
PR	17-JUN-1999;	99US-0139492.
PR	18-JUN-1999;	99US-0139454.
PR	18-JUN-1999;	99US-0139455.
PR	18-JUN-1999;	99US-0139456.
PR	18-JUN-1999;	99US-0139457.
PR	18-JUN-1999;	99US-0139458.
PR	18-JUN-1999;	99US-0139459.
PR	18-JUN-1999;	99US-0139460.
PR	18-JUN-1999;	99US-0139461.
PR	18-JUN-1999;	99US-0139462.
PR	18-JUN-1999;	99US-0139463.
PR	18-JUN-1999;	99US-0139750.
PR	21-JUN-1999;	99US-0139817.
PR	22-JUN-1999;	99US-0139899.
PR	23-JUN-1999;	99US-0140353.
PR	23-JUN-1999;	99US-0140354.
PR	24-JUN-1999;	99US-0140695.
PR	28-JUN-1999;	99US-0140823.
PR	29-JUN-1999;	99US-0140991.
PR	30-JUN-1999;	99US-0141287.
PR	01-JUL-1999;	99US-0141842.
PR	01-JUL-1999;	99US-0142154.
PR	02-JUL-1999;	99US-0142055.
PR	06-JUL-1999;	99US-0142390.
PR	08-JUL-1999;	99US-0142803.
PR	09-JUL-1999;	99US-0142920.
PR	12-JUL-1999;	99US-0142977.
PR	13-JUL-1999;	99US-0143542.
PR	14-JUL-1999;	99US-0143624.
PR	15-JUL-1999;	99US-0144005.
PR	16-JUL-1999;	99US-0144085.
PR	16-JUL-1999;	99US-0144086.
PR	19-JUL-1999;	99US-0144325.
PR	19-JUL-1999;	99US-0144331.
PR	19-JUL-1999;	99US-0144332.
PR	19-JUL-1999;	99US-0144333.

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PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144352.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 22-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
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PR 05-AUG-1999; 99US-0147360.
PR 06-AUG-1999; 99US-0147303.
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PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
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PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158222.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.

PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
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PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 57.1%; Score 1297; DB 21; Length 485;
Best Local Similarity 56.9%; Pred. No. 2.3e-125;
Matches 269; Conservative 52; Mismatches 104; Indels 48; Gaps 6;

QY 7 YKVADIGLAAGWKALDIAENEMPGLMRMRYRSASKPLKGARIAGCLHMTVETAVLIET 66
DB 14 YVKDLSQADFQRLERIEIAEVEPMGLMACRABFGSKPPAGARISGSLHMTIQTAVLIET 73
QY 67 LVTLGAEVQWSSCNIFSTQNHAAAIKAKGIPVYAWKGETDEYLCWICIBQTLTYFKD--GP 124
DB 74 LTALGAEVWCSNIFSTQDHAAAIARDSAVFAWKGETLEEYWWCTERCIDWGEAGGP 133
QY 125 LNMILDDGGDLNLH-----TKY 143
DB 134 -DLIVDDGGDATLLIHGKABEEYEKTKIPDPESTDNABFKIVLTIIRDGLKADPKKY 192
QY 144 POLLFGIRISBETTTGVHNLKMWANGILKVPAINVNDSTKSKFDNLYGCRESLIDGI 203
DB 193 RKMKERLVGVSEETTTGVKRLYQMETGALLFPAINVNDSTKSKFDNLYGCRHSLPDGL 252
QY 204 KBATDVIAGKVVAVVAGYGVKGCAQALRGFGARVITEIDPINALQAAMEGYEYTTMD 263
DB 253 MRATDVIAGKVVAVVAGYGVKGCAALKQAGARVITEIDPICALQALMEGLQVLPLE 312
QY 264 EACQEGNIFVTTTCIDILGRHFPQMKDDAIVCNIGHFDVIDVKWLN-NAVEKWNK 322
DB 313 DVVSEADIFVTTGNKDIIMVDHMRKKNNAIVCNIGHFDNEIDMLGLEYTPGVKRITIK 372
QY 323 POWDRYRL-KNGRRRIILAEGLVNLGCAWGHPSFVMSNFTNQVMAQIELWTHPD--KV 379
DB 373 POTDRVFPETNTGIIIVLAEGRLMNLGCATGHPSPVMSCSFTNQVIAQLWKEKSSGKY 432
QY 380 PVGVHFLPKKLDEAAVAEHLGKLNKLTKLTEKQAOYLGMSCDGPFPKPDHYRY 432
DB 433 EKKVVVLPKHLDEKVAALHLGLGAKLTKLTKSQADYISVPTEGPKPAHYRY 485

RESULT 7
AAG34059
ID AAG34059 standard; Protein; 510 AA.
XX
AC AAG34059;
XX
DT 18-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 41386.
XX
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridization assay; genetic mapping; gene expression control; promoter;
XX termination sequence; corn.
OS Zea mays subsp. mays.
XX EP1033405-A2.
PN 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
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PR 04-JUN-1999; 99US-0137502.
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PR 08-JUN-1999; 99US-0138094.
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PR 22-JUN-1999; 99US-0139899.
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PR 28-JUN-1999; 99US-0140823.
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PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
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PR 21-JUL-1999; 99US-0145086.
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PR 28-JUL-1999; 99US-0145951.
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PR 13-AUG-1999; 99US-0148565.
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PR 17-AUG-1999; 99US-0149175.
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PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.

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PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
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PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 57.1%; Score 1297; DB 21; Length 510;
Best Local Similarity 56.9%; Pred. No. 2.5e-125;
Matches 269; Conservative 52; Mismatches 104; Indels 48; Gaps 6;

QY 7 YKVADIGLAAGRKALDIAENEMPGLMRMRYRSASKPLKGARIAGCLHMTVETAVLIET 66
DB 39 YKVKDLSQADFGFLELEIAEVENPGLMACRAEFGPSKPFAGARISGSLHMTIQTAVLIET 98
QY 67 LVTLGAEVQWSSCNIFSTQNHAAATAKAGIPVYAWKGETDBEYLWCIEOTLYFXD--CP 124
DB 99 LTLGAEVWVSCNIFSTQDHAAALARDSAAVFAWKGETLBEYMWCTERCCLDWGAGGP 158
QY 125 LNMILDGGLDNLNLIH-----TKY 143
DB 159 -DLIVDDGGDATLLIHGKVAEEYEKTKIPDPESTDNAEFKIVLTIIRDGLKADPKY 217
QY 144 POLLPOIRGISBETTTGVNLYKMMANGILKVPAINVNDSVTKSPDNLYGCRSLIDGI 203
DB 218 RMKRELVGVBSETTTGVKRLYQMOBTGALLFPAINVNDSVTKSPDNLYGCRHSLPDGL 277
QY 204 KRATDVIAGKAVVAGYGVGKGAQALRGFGARVITTEIDPINALQAAMEGYETWTD 263
DB 278 MRATDVIAGKAVVAGYGVGKGAQALRGFGARVITTEIDPINALQAAMEGYETWTD 337
QY 264 EACQEGNIFVTTTGGCIDIILGRHFEQMKODAIVCNIGHFDVEIDVKWLNE-NAVEKVNIK 322

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DB 338 DVVSEADIFVTTTNGKDIIMVDMRKMKNVAIVCNIGHFDNEIDMLGLSTYPCVKRITIK 397
QY 323 PQVDYRL-KNGRRILLAEGLVNLGCMGHPSPFVMSNSFTNOVMAQIELWTHPD--KY 379
DB 398 PQTDRWVPETNTGTIIVLAEGRLMNLGCATGHPSPFVMSCSFTNQVIAQLLEWKESSGKY 457
QY 380 PVGVHFLPKKLDEAAEAHLGKLVNKLTKLTKEQAYLGMSCDGPFPKDPHYRY 432
DB 458 EKKVTVLPKHLDEKVAALHLGKLVNKLTKLTKSQADYISVPIEGPKPAHYRY 510

RESULT 8
AAR26500
ID AAR26500 standard; Protein; 486 AA.
XX AAR26500;
XX
DT 10-MAR-1993 (first entry)
XX
DE Prod. of Nicotiana tabacum gene expressing at floral differentiation.
XX Flower; induction.
XX Nicotiana tabacum.
XX JP04258292-A.
PD 14-SEP-1992.
XX
PF 14-FEB-1991; 91JP-0020702.
XX
PR 14-FEB-1991; 91JP-0020702.
XX
PA (NISR) JAPAN TOBACCO INC.
XX
XX WPI; 1992-354683/43.
DR N-PSDB; AAQ29419.
XX
XX Gene expressing at floral differentiation for flowering control -
PT obtd. from culture of floral axis epithelium cells of Nicotiana
PT tabacum, for introduction into other plants
XX
PS Disclosure; Page 6; 8pp; Japanese.
XX
CC The protein sequence was deduced from the DNA sequence of a clone
CC obtd. by screening a cultured epithelial axis cDNA library with probes
CC from cultured and untreated mRNA. The clone obtd. expressed its
CC protein only at floral differentiation. The gene can be introduced
CC into other plants or can be suppressed by an antisense technique for
CC the control of flowering of plants.
XX
SQ Sequence 486 AA;
Query Match 57.1%; Score 1296; DB 13; Length 486;
Best Local Similarity 56.6%; Pred. No. 3e-125;
Matches 267; Conservative 55; Mismatches 104; Indels 46; Gaps 5;

QY 7 YKVADIGLAAGRKALDIAENEMPGLMRMRYRSASKPLKGARIAGCLHMTVETAVLIET 66
DB 15 YKVKDMSQADFGFLEIAEVENPGLMACRTEFGPSQPFKAGITGSLHMTIQTAVLIET 74
QY 67 LVTLGAEVQWSSCNIFSTQNHAAATAKAGIPVYAWKGETDBEYLWCIEOTL-YFKDGPL 125
DB 75 LTLGAEVWVSCNIFSTQDHAAALARDSAAVFAWKGETLQEYVWCTERCCLDWGPGGPG 134
QY 126 LNMILDGGLDNLNLIH-----TKYP 144
DB 135 DLIVDDGGDATLLIHGKVAEEFAKNGTIPDPNSTDNAEFQVLVTIIKESLKTPLKYT 194
QY 145 QLLPOIRGISBETTTGVNLYKMMANGILKVPAINVNDSVTKSPDNLYGCRSLIDGIK 204
DB 195 KMRELVGVBSETTTGVKRLYQMOANGTLLFPAINVNDSVTKSPDNLYGCRHSLPDGLM 254

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	Query Match	56.9%; Score 1292; DB 21; Length 485;
	Best Local Similarity	56.3%; Pred. No. 7.7e-125;
	Matches 267; Conservative	55; Mismatches 102; Indels 50; Gaps
QY	7 YKVADICLAAGRKALDIAENEMPGLMRMRYSASKPLKGARIACIACIHHMTVETAVLIET 66	
DB	14 YKVKDMSQADFGRLELEAEVMPGLMACRTFEPSPFGKARITGSLHMTTQTAVLIET 73	
QY	67 LVTLGAEVQWSSCNIFSTQNHAATAKAGIPYAWKGETDEBYLCIBOTL-YFKDGPL 125	
DB	74 LTALGAEVRWCSCNIFSTQDHAAAAIARDSAAVPAWKGETLQBYWWCTERALDWGGCGP 133	
QY	126 NMILDDGGDLTNLIH-----TKYP 144	
DB	134 DLIVDDGGDATLLIHGVKAEEIFEKTGTQVPDPTSTDNPFEQIVLSIIKEGLQVDPKYH 193	
QY	145 QLLPGIRGISSETTGVHNLYKMANGILKVPAINVNDSVTSKFDNLVGCRESLIDGIK 204	
DB	194 KMKERLVGVSEETTGVKRLYQMONGTLFPAINVNDSVTSKFDNLVGCRESLDPGLM 253	
QY	205 RATDVMIAGVVAVGVGDKCAOALRGFGARVIITEIDPINALQAAMEGYEVTTMBE 264	
DB	254 RATDVMIAGKVAIVCYGDVGKCAAMKTAGARVIVTEIDPICALLMEGLQVUTLSD 313	
QY	265 ACQEGNIFVTTTCIDIILGRHFPEOMKDDAIVCNIIGHFDVEIDVKWLNE-NAVEKNINRP 323	
DB	314 VVSEADIFVTTTGKDIIIMVDMHKMKNNAIVCNIGHFDNEIDMLGLETPGVKRITIKP 373	
QY	324 QVDRY---RLKNGRIILLAEGRVLNIGCAMGHPSFMNSFTNQVMAQIELMTH--PDK 378	
DB	374 QTDRWVPETKAG--IIVLAEGRLMNLCATGHPFSVMSCSFTNQVIAQLMELMNERKASGK 431	
QY	379 YPVGVHELPKKLDEANVAEHLGKLVKLTGKTEKQAYLGMSCDGPKPDPHYRY 432	
DB	432 YEKKVYVLPKHLDEKVALDLHGKLGARLTKLKSKQSDSYVSPIEGPYKPPHYRY 485	
	RESULT 10	
ID	AAG40085 standard; Protein; 508 AA.	
XX	AAG40085;	
DT	18-OCT-2000 (first entry)	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 49690.	
KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
XX	termination sequence.	
OS	Arabidopsis thaliana.	
PN	EP1033405-A2.	
PD	06-SEP-2000.	
PF	25-FEB-2000; 2000EP-0301439.	
PR	25-FEB-1999; 99US-0121025.	
PR	05-MAR-1999; 99US-0123180.	
PR	09-MAR-1999; 99US-0123548.	
PR	23-MAR-1999; 99US-0125788.	
PR	25-MAR-1999; 99US-0126264.	
PR	29-MAR-1999; 99US-0126785.	
PR	01-APR-1999; 99US-0127462.	
PR	06-APR-1999; 99US-0128234.	
PR	08-APR-1999; 99US-0128714.	
PR	16-APR-1999; 99US-0129845.	
PR	21-APR-1999; 99US-0130077.	
PR	23-APR-1999; 99US-0130449.	
PR	23-APR-1999; 99US-0130510.	

PR	23-APR-1999;	99US-01130891.	PR	20-JUL-1999;	99US-01448084.
PR	28-APR-1999;	99US-0131449.	PR	21-JUL-1999;	99US-01448114.
PR	30-APR-1999;	99US-0132048.	PR	21-JUL-1999;	99US-0145086.
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PR	04-MAY-1999;	99US-0132484.	PR	22-JUL-1999;	99US-0145085.
PR	05-MAY-1999;	99US-0132485.	PR	22-JUL-1999;	99US-0145087.
PR	06-MAY-1999;	99US-0132486.	PR	22-JUL-1999;	99US-0145089.
PR	06-MAY-1999;	99US-0132487.	PR	22-JUL-1999;	99US-0145192.
PR	07-MAY-1999;	99US-0132863.	PR	23-JUL-1999;	99US-0145145.
PR	11-MAY-1999;	99US-0134256.	PR	23-JUL-1999;	99US-0145218.
PR	14-MAY-1999;	99US-0134218.	PR	23-JUL-1999;	99US-0145218.
PR	14-MAY-1999;	99US-0134219.	PR	26-JUL-1999;	99US-0145224.
PR	14-MAY-1999;	99US-0134221.	PR	26-JUL-1999;	99US-0145276.
PR	14-MAY-1999;	99US-0134370.	PR	27-JUL-1999;	99US-0145913.
PR	18-MAY-1999;	99US-01343768.	PR	27-JUL-1999;	99US-0145918.
PR	19-MAY-1999;	99US-0134941.	PR	27-JUL-1999;	99US-0145919.
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QY	67	LVTLGAEVQWSCNIFSTQNHAAAAIAKAGIPYAWKGETDEBYLWCIEQTL-YFKDGPL 125
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QY	126	NMILDDGGDLTNLIH-----	-----TKYP 144
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QY	145	QLLPGIRGISERTTGVHNLVYKWMANGILKVPAINVNDSTVTKSKFDNLYGCCRESLIDGIK 204	
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QY	205	RATDVMIAGKAVAVAGYGDVHGKCAQALRGFGARVITTEIDPINALQAAMEGVYVTTMDE 264	
Db	254	RATDVMIAGKAVICGYGDVGKGCACAAAMKTAGARVITTEIDPICALQALMEGLQVLTLED 313	
QY	265	ACQEGNIPVTTTGCIDILGRHFEQMKDDAIVCNIGHEDVEIDVKWLINE-NAVEKVNIKP 323	
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QY	324	QVDRYRLKN-GRRIILLAEGRVLNLCAMGHPSPVMSNSFTNQVMAQIELWTHPD--KYP 380	
Db	374	QTRWVFPDTSGLIIVLAEGRLMNLGCATGHPSPVMSCSFTNQVIAQLELWNEKSSGKYE 433	
QY	381	GVHFLPKKLDVAABAHKLNVKLTKEKQAQYLGMSCDGPPKPDHYRY 432	
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XX	DT 18-OCT-2000 (first entry)		
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XX	Arabidopsis thaliana.		
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PN	06-SEP-2000.		
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Query Match          56.1%; Score 1274; DB 21; Length 497;
Best Local Similarity 55.5%; Pred. No. 6e-123;
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QY 67 LVTLGAEVOWSSCNIFSTQNHAAAAIAKAGIPYAWKGETDEBYLWCIEOTL-YFKDGPL 125
Db 86 LTFALGAEVRWCSCNIFSTQDHAHAARDAASAVFANKGETLQYWNCTERALDWGPGGP 145
QY 126 NMLDDGGDLNLIH-----TKYP 144
Db 146 DLIVDDGGDALLIHGKVAEEIFAKNGTTPDPTSTDNPEFQIVLSIIKQGLQVDPKXK 205
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XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 49692.
XX DE Arabidopsis thaliana.
XX DE Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
XX PR 09-MAR-1999; 99US-0123548.
XX PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
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PR 16-APR-1999; 99US-0129845.
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Qy 134 DLTNLIH-----TKYPQLLPIRG 152
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